

Result No.	Query	Score	Match	Length	DB ID	Description
1	1836	99.7	352	2	A43113	chemokine (C-C) receptor, 5 - human
2	1359	73.8	360	2	JC2443	N;Alternate names: C-C CKR-5; CCR5
3	1219	66.2	374	2	J38450	C;Species: Homo sapiens (man)
4	1059	57.5	355	2	A45177	C;Date: 12-Jul-1996 #sequence revision 12-Jul-1996 #text Change 20-Jun-2000
5	1011.5	54.9	355	2	I49339	C;Accession: A43113; S71808; A58834; A58832; G02653; A51372
6	1003.5	54.5	359	2	I49341	R;Samson, M.; Liebert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Saragosti M.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Vassart, G.; Nature 332, 722-725, 1996
7	936.5	50.9	355	2	G02436	A;Title: Molecular cloning and functional expression of a new human CC-chemokine receptor 5; A;Reference number: A43113; MUID:96241590; PMID:8639485
8	914	49.6	360	2	JC57160	A;Molecule type: mRNA
9	901	48.9	360	2	JC4587	A;Residues: 1-352 <SAM1>
10	832	45.2	383	2	S55594	A;Cross-references: GB:X9933; NID:91524062; PID:CAA6776.1; PID:91524063
11	802.5	43.6	356	2	I49340	R;Samson, M.; Liebert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Saragosti M.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Vassart, G.; Nature 332, 722-725, 1996
12	751.5	40.8	355	2	JC5067	A;Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles of the CCR5 gene; A;Accession number: S71808; PMID:875144
13	717	38.9	354	2	I58186	A;Status: nucleic acid sequence not shown; not compared with conceptual translation
14	675.5	36.7	355	2	JC4304	A;Molecule type: DNA
15	670	36.4	344	2	JC5942	A;Residues: 1-206;207-230 <SAM2>
16	562	30.5	378	2	B55735	A;Status: nucleic acid sequence not shown; not compared with conceptual translation
17	560	30.4	378	2	A55735	A;Molecule type: DNA
18	554	30.1	369	2	JC5068	A;Residues: 1-184 /IKDSHLAGPAAAGHGHLLGPNPKNSASVSK/ <SAM3>
19	548	23.8	378	2	A45680	A;Note: this frameshift mutation results in a non-functional receptor but confers a deg
20	542	23.4	333	2	I65989	nd may have had a selective advantage by conferring resistance to Yersinia plague infec
21	520	28.2	360	2	A53611	R;Combaudiere, C.; Ahuja, S.K.; Tiffany, H.L.; Murphy, P.M.
22	516.5	28.1	359	2	A48921	J. Leukoc. Biol. 60, 147-152, 1996
23	514	27.9	378	2	JQ1231	A;Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes
24	513.5	27.9	358	2	A53752	R;Combaudiere, C.
25	505.5	27.5	350	2	A39445	Submitted to the BMBL Data Library, May 1996
26	505.5	27.5	367	2	JE0349	A;Reference number: H01541
27	504.5	27.4	350	2	JN0621	A;Accession: A58832
28	501	27.2	352	2	G0048	A;Cross-references: GB:EMBL/DDJB
29	501	27.2	352	2	A45747	A;Status: translated from GB:EMBL/DDJB

Copyright (c) 1993 - 2005 Compugen Ltd.

CM protein - protein search, using sw model

Run on: October 3, 2005, 07:42:35 ; Search time 28 Seconds
(without alignments)
1209.582 Million cell updates/sec

Title: US-10-700-313-2
Perfect score: 1841
Sequence: 1 MDYQSSPIYDINYTSEPC.....ERASSVYTRSTGEQEISVGL 352

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

Database : PIR 79/*
1: pir1/*
2: pir2/*
3: pir3/*
4: pir4/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	1836	99.7	352	2	A43113	chemokine (C-C) receptor, 5 - human
2	1359	73.8	360	2	JC2443	chemokine (C-C) receptor, 5 - human
3	1219	66.2	374	2	J38450	chemokine (C-C) receptor, 5 - human
4	1059	57.5	355	2	A45177	chemokine (C-C) receptor, 5 - human
5	1011.5	54.9	355	2	I49339	macrophage inflammatory protein-1 alpha receptor
6	1003.5	54.5	359	2	I49341	chemokine (C-C) receptor, 5 - human
7	936.5	50.9	355	2	G02436	MIP-1 alpha receptor
8	914	49.6	360	2	JC57160	chemokine (C-C) receptor, 5 - human
9	901	48.9	360	2	JC4587	chemokine (C-C) receptor, 5 - human
10	832	45.2	383	2	S55594	protein-coupled receptor, 5
11	802.5	43.6	356	2	I49340	MIP-1 alpha receptor
12	751.5	40.8	355	2	JC5067	G protein-coupled receptor, 5
13	717	38.9	354	2	I58186	probable G protein-coupled receptor, 5
14	675.5	36.7	355	2	JC4304	orphin G protein-coupled receptor
15	670	36.4	344	2	JC5942	chemokine receptor, 5
16	562	30.5	378	2	B55735	lymphocyte-specific protein-coupled receptor
17	560	30.4	378	2	A55735	G protein-coupled receptor
18	554	30.1	369	2	JC5068	G protein-coupled receptor
19	548	23.8	378	2	A45680	G protein-coupled receptor
20	542	23.4	333	2	I65989	interleukin-8 receptor
21	520	28.2	360	2	A53611	interleukin-8 receptor
22	516.5	28.1	359	2	A48921	interleukin-8 receptor
23	514	27.9	378	2	JQ1231	interleukin-8 receptor
24	513.5	27.9	358	2	A53752	interleukin-8 receptor
25	505.5	27.5	350	2	A39445	interleukin-8 receptor
26	505.5	27.5	367	2	JE0349	interferon-inducible protein (IFI44)-like protein
27	504.5	27.4	350	2	JN0621	G protein-coupled receptor
28	501	27.2	352	2	G0048	fusin (LUSTRA) - chemokine receptor
29	501	27.2	352	2	A45747	neuropeptide Y receptor, 5

ALIGNMENTS

RESULT 1

A43113
Chemokine (C-C) receptor, 5 - human
N;Alternate names: C-C CKR-5; CCR5
C;Species: Homo sapiens (man)
C;Accession: A43113; S71808; A58834; A58832; G02653; A51372
R;Samson, M.; Liebert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Saragosti M.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Vassart, G.; Nature 332, 722-725, 1996
Biochemistry 35, 3362-3367, 1996
A;Title: Molecular cloning and functional expression of a new human CC-chemokine receptor 5; A;Reference number: A43113; MUID:96241590; PMID:8639485
A;Accession: A43113
A;Molecule type: mRNA
A;Residues: 1-352 <SAM1>
A;Cross-references: GB:X9933; NID:91524062; PID:CAA6776.1; PID:91524063
R;Samson, M.; Liebert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Saragosti M.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Vassart, G.; Nature 332, 722-725, 1996
Biochemistry 35, 3362-3367, 1996
A;Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles of the CCR5 gene; A;Accession number: S71808; PMID:875144
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-206;207-230 <SAM2>
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-184 /IKDSHLAGPAAAGHGHLLGPNPKNSASVSK/ <SAM3>
A;Note: this frameshift mutation results in a non-functional receptor but confers a deg
A;Cross-references: GB:X9933; NID:91524062; PID:CAA6776.1; PID:91524063
R;Combaudiere, C.; Ahuja, S.K.; Tiffany, H.L.; Murphy, P.M.
J. Leukoc. Biol. 60, 147-152, 1996
A;Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine receptor 5; A;Reference number: A58832; MUID:96249970; PMID:8699119
A;Accession: A58832
A;Molecule type: mRNA
A;Residues: 1-352 <COM1>
A;Cross-references: GB:EMBL/DDJB
A;Status: translated from GB:EMBL/DDJB
A;Molecule type: mRNA
A;Residues: 1-89, L' - 91-352 <COM2>
R;Combaudiere, C.
R;Report, C.J.; Geissler, J.; Schweickart, V.L.; Charo, I.F.
J. Biol. Chem. 271, 17161-17166, 1996
A;Title: Molecular cloning and functional characterization of a novel human CC chemokine receptor 5; A;Reference number: A58833; MUID:96291862; PMID:8663314
A;Reference number: A58833

A; Accession: A58833	A; Molecular type: mRNA
A; Residues: 1-352 >PAP>	
A; Cross-references: GB:U54994; NID:91457945; PIDN: AAC05098.1; PID:91457946	
C; Comment: This is a receptor for chemokines MIP-1alpha (see PIR: I30574), MIP-1beta (see PIR: I30574), bind to a complex of chemokine C; Genetics:	
A; Gene: GRB: CMKBR5; CCRS5; CCR5; CC-CKR-5; CKR5; ChemR13	
A; Cross-references: GDB:1230510; OMIM:601373	
A; Map position: 3p21-3p21	
C; Function:	G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RANTES
A; Note: probably acts to control granulocyte proliferation and differentiation	
C; Superfamily: vertebrate rhodopsin	
C; Keyword: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane	
F; 32-56/Domain: transmembrane #status predicted <TM1>	
F; 67-87/Domain: transmembrane #status predicted <TM2>	
F; 112-166/Domain: transmembrane #status predicted <TM3>	
F; 133-218/Domain: transmembrane #status predicted <TM4>	
F; 236-257/Domain: transmembrane #status predicted <TM5>	
F; 285-300/Domain: transmembrane #status predicted <TM6>	
F; 269, 101-178/Disulfide bonds: #status predicted <TM7>	
F; 28/Binding site: carbohydrate (Asn) (covalent) #status predicted	
F; 336, 337, 342/Binding site: phosphate (Ser) (covalent) #status predicted	
F; 340, 343/Binding site: phosphate (Thr) (covalent) #status predicted	
Query Match Score 99.1%; Best Local Similarity 99.7%; Pred. No. 7 2e-143; Matches 351; Conservative 0; Missmatches 1; Indels 0; Gaps 0;	Length 352;
Qy 1 MDYQVSSPIYDINYTTSEPCOKINVQIAARLLPPPLSVPFVGIVENMLVILILINCKR 60	
Db 1 MDYQVSSPIYDINYTTSEPCOKINVQIAARLLPPPLSVPFVGIVENMLVILILINCKR 60	
Qy 61 LKSMTDIYLNAISDLFELLTVPTWVYLAQWDGNTMCQLLTGLPFIGFSGIFFI 120	
Db 61 LKSMTDIYLNAISDLFELLTVPTWVYHAARAQWDGNTMCQLLTGLPFIGFSGIFFI 120	
Qy 121 LLTIDRYLAVVHAFVALKARTTGFYTTSVITWVVAFAASLPGLIITRSQKRGHLHTCSSL 180	
Db 121 LLTIDRYLAVVHAFVALKARTTGFYTTSVITWVVAFAASLPGLIITRSQKRGHLHTCSSL 180	
Qy 181 HPPYSQQYQFWQNFTQTLKIVLGLVLPLVMVICYSGLKTLLRCNEKKHRRAVRLIFTI 240	
Db 181 HPPYSQQYQFWQNFTQTLKIVLGLVLPLVMVICYSGLKTLLRCNEKKHRRAVRLIFTI 240	
Qy 241 MIVYFLDWAPVNVLINTFQEFGIQLNCSSSNRLQAMQVTETLGMTHCCINPIIAFV 300	
Db 241 MIVYFLDWAPVNVLINTFQEFGIQLNCSSSNRLQAMQVTETLGMTHCCINPIIAFV 300	
Qy 301 GEKFRRNLLVFQKHIAKRFCKCCS1IQQEAPERASSVYTRSTGEQTISVGL 352	
Db 301 GEKFRRNLLVFQKHIAKRFCKCCS1IQQEAPERASSVYTRSTGEQTISVGL 352	
RESULT 2	JC2443
A; Residues: 1-360 <PAP>	Chemokine (C-C) receptor 2, splice form B - human
A; Cross-references: UNIPROT: P41597; DDBJ:D29984; NID:9531246; PIDN:BAA06253.1; PID:9531243	Alternative names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chemoattractant protein 1 (man)
C; Species: Homo sapiens (man)	
C; Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004	
R; Tamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.	
Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994	
A; Title: cDNA cloning and functional expression of a human monocyte chemoattractant protein 2	
A; Reference number: JC2443; MUID:94324942; PMID:8048929	
A; Accession: JC2443	
A; Molecular type: mRNA	
A; Residue: 1-360 <PAP>	

A1:Title: Molecular cloning and functional expression of two monocyte chemoattractant protein-1 genes
A1:Reference: number: A53477; MUID:9419521; PMID:8146186
A1:Accession: I38463
A1:Status: preliminary
A1:Molecule type: mRNA
A1:Residues: 1-360 <RES>
A1:Cross-references: EMBL:U03905; NID:9472557; PIDN:AAA19120.1; PID:9472558
C1:Genetics:
A1:Gene: GDB:CMKBR2
A1:Cross-references: GDB:337364; OMIM:601267
A1:Map position: 3p21-3p21
C1:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane
C1:Superfamily: vertebrate rhodopsin
C1:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane
F1:43-70/Domain: transmembrane #status Predicted <TM1>
F1:81-100/Domain: transmembrane #status Predicted <TM2>
F1:115-136/Domain: transmembrane #status Predicted <TM3>
F1:154-178/Domain: transmembrane #status Predicted <TM4>
F1:207-226/Domain: transmembrane #status Predicted <TM5>
F1:244-268/Domain: transmembrane #status Predicted <TM6>
F1:287-310/Domain: transmembrane #status Predicted <TM7>
F1:14/Binding site: carbohydrate (Asn) (covalent) #status Predicted
F1:113-190/Disulfide bonds: #status Predicted

C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane
 P;44-68/Domain: transmembrane #status predicted <TM1>
 P;79-99/Domain: transmembrane #status predicted <TM2>
 P;115-136/Domain: transmembrane #status predicted <TM3>
 P;154-178/Domain: transmembrane #status predicted <TM4>
 P;208-226/Domain: transmembrane #status predicted <TM5>
 P;244-265/Domain: transmembrane #status predicted <TM6>
 P;292-309/Domain: transmembrane #status predicted <TM7>
 P;14/Birding site: carbohydrate (Asn) (covalent) #status predicted
 P;32-277,113-190/Disulfide bonds: #status predicted
 Query Match 66.2%; Score 1219; DB 2; Length 374;
 Best Local Similarity 76.0%; Pred. No. 2.3e-92;
 Matches 234; Conservative 27; Mismatches 35; Indels 12; Gaps 3;

Qy 10 YDINTYTSSEPCOKINVQIAARLLPLPSLYIFOFVGNMLVILINCKRLKSMTDIVL 69
 Db 24 FDYDY--GAPCHKFVDQIAQLLPLPSLYIFRGVGNMLVILINCKRLKCLTDIVL 81

Qy 70 INLAISDLFFLTLTVFPAWHLAQAQDFGNTMCQLLTGLYPIGFSSGIFFLILLTIDRVL 129
 Db 82 INLAISDLFFLTLTVFPAWHLAQAQDFGNTMCQLLTGLYPIGFSSGIFFLILLTIDRVL 141

Qy 130 VHVAFALKARTVTFEVVTSVITWVAVFASLPGLIITFRSOKEGHLYTCSSHFPYSQOF 189
 Db 142 IWHVAFALKARTVTFEVVTSVITWVAVFASLPGLIITFRSOKEDSVVCPYFP---RG 197

Qy 190 WKNFOTLKIVLGLVPLIVVYSGILKTLRERNEKKRHRRAVRLIFTIMITYFLFWA 249
 Db 198 WNNFHFTIMRNLLGVLPLIVVYSGILKTLRERNEKKRHRRAVRLIFTIMITYFLFWT 257

Qy 250 PYNIVLILANTFOEFFGLANNCSSSNRLDQAMQTEFLGMTHCCINPILYAFVGKEPRNLL 309
 Db 258 PYNIVLILANTFOEFFGLANNCSSSNRLDQAMQTEFLGMTHCCINPILYAFVGKEFRSLP- 316

Qy 310 VFFQKHIA 317
 Db 317 ---- HIA 319

RESULT 4

A45177 Chemokine (C-C) receptor 1 - human
 N;Alternative names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor
 C;Species: Homo sapiens (man)
 C;Accession: A45177; 155671
 R;Note, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.
 Cell 72, 415-425, 1993
 A;Title: Molecular cloning, functional expression, and signaling characteristics of a C-C chemokine receptor gene.
 A;Reference number: A45177; MUID:3161416; PMID:7679328
 A;Accession: A45177
 A;Molecule type: mRNA
 A;Residues: 1-355 <RES>
 A;Cross-references: UNIPROT:P32246; GB:L10918; NID:g292416; PID:9292417
 A;Experimental source: HL60 cells
 A;Note: sequence extracted from NCBI backbone (NCBIP:124876)
 R;Gao, J.
 J. Exp. Med. 177, 1421-1427, 1993
 A;Title: Structure and functional expression of the human macrophage inflammatory 1 alpha
 A;Reference number: 155671; MUID:93240122; PMID:7683036
 A;Accession: 155671
 A;Status: Preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-355 <RES>
 A;Cross-references: GB:L10918; NID:g292416; PID:AAA36543.1; PID:g292417
 C;Genetics: GDB:CMKBR1; CMKR-1
 A;Cross-references: GDB:138446; OMIM:601159
 A;Map position: 3p21-3p21
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein; t;

P;36-60/Domain: transmembrane #status predicted <TM1>
 P;71-91/Domain: transmembrane #status predicted <TM2>
 P;108-129/Domain: transmembrane #status predicted <TM3>
 P;147-171/Domain: transmembrane #status predicted <TM4>
 P;205-223/Domain: transmembrane #status predicted <TM5>
 P;240-264/Domain: transmembrane #status predicted <TM6>
 P;268-305/Domain: transmembrane #status predicted <TM7>
 P;5/Binding site: carbohydrate (Asn) (covalent) #status predicted
 P;24-273,106-183/Disulfide bonds: #status predicted
 P;345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
 Query Match 57.5%; Score 1059; DB 2; Length 355;
 Best Local Similarity 56.4%; Pred. No. 2.7e-79;
 Matches 198; Conservative 59; Mismatches 88; Indels 6; Gaps 4;

Qy 2 DYQVSSPIDINYTSSEPCOKINVQIAARLLPLPSLYIFFGVGNMLVILINCKRL 61
 Db 9 DYDTT---EFDYGDATDPCQVNERRAGQQLPPLPSLYIFVGVGNMLVILVQYKRL 65

Qy 62 KSMTDIYLNLNAISDLFFLTLTVFPAWHLAQAQDFGNTMCQLLTGLYPIGFSSGIFFI 120
 Db 66 KNMTSIYLNLAISDLFFLTLTVFPAWHLAQAQDFGNTMCQLLTGLYPIGFSSGIFFI 125

Qy 121 LLTIDRYLAVHAYAFAALKARTVTFEVVTSVITWVAVFASLPGLIITFRSOKEGHLYTCSS 180
 Db 126 LLTIDRYLAVHAYAFAALKARTVTFEVVTSVITWVAVFASLPGLIITFRSOKEGHLYTCSS 185

Qy 181 HFPPSQYQFWKNFQTLKIVLGLVPLIVVYSGILKTLRERNEKKRHRRAVRLIFTI 240
 Db 186 HFPPESLRWKLPDAKLNLLGVLPLIVVYSGILKTLRERNEKKRHRRAVRLIFTI 244

Qy 241 MIVVFLFWAPYNTVLLNTFOQEFFGLANNCSSSNRLDQAMQTEFLGMTHCCINPILYAFV 300
 Db 245 MIVVFLFWAPYNTVLLNTFOQEFFGLANNCSSSNRLDQAMQTEFLGMTHCCINPILYAFV 304

Qy 301 GEKPRYLLVVFQGHIAKRFCKCCSIIFOOQAPRASSYVTRSTQEISVG 351
 Db 305 GERRPKYLRQLFHERRVAVHLVKNLPLFSYDRLEVSST-SPSTEHELSAG 354

RESULT 5

I43339 macrophage inflammatory protein-1 alpha receptor - mouse
 C;Species: Mus musculus (house mouse)
 C;Accession: I43339
 R;Gao, J.L.; Murphy, P.M.
 J. Biol. Chem. 270, 1794-17501, 1995
 A;Title: Cloning and differential tissue-specific expression of three mouse beta chemokines
 A;Reference number: 149339; MUID:95340546; PMID:7542241
 A;Accession: I49339
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-355 <RES>
 A;Cross references: UNIPROT:P51675; EMBL:U28404; NID:g881547; PID:AAA89153.1; PID:9881
 C;Superfamily: vertebrate rhodopsin

Query Match 54.9%; Score 1011.5; DB 2; Length 355;
 Best Local Similarity 55.8%; Pred. No. 2.1e-75; Mismatches 55; Indels 3; Gaps 3;
 Matches 191; Conservative 55; Mismatches 93; Indels 3; Gaps 3;

Qy 11 DINYYTSSEPCQKINVQIAARLLPLPSLYIFFGVGNMLVILINCKRLKSMTDIYL 70
 Db 15 EFYGDSTPQCQTKVAVRAGAGLIPPLSVFVIGGVGNMLVILMQHRRQLQSMTSILF 74

Qy 71 NLASDUFFLTLTVFPAWHLAQAQDFGNTMCQLLTGLYPIGFSSGIFFI 129
 Db 75 NLASDUFFLTLTVFPAWHLAQAQDFGNTMCQLLTGLYPIGFSSGIFFI 134

Qy 130 VHVAFALKARTVTFEVVTSVITWVAVFASLPGLIITFRSOKEGHLYTCSSHFPYSQOF 189
 Db 135 VHVAFALKARTVTFEVVTSVITWVAVFASLPGLIITFRSOKEGHLYTCSSHFPYSQOF 194

Qy	190	WNFOTLKVILGLVLPPLAMVICYSGILKTLRCKRKRAVLRLFTIMIVYFLWVA 249	A; Cross-references: UNIPROT:P51677; EMBL:U49727; NID:gi477560; PID:gi477560; PID:914
Db	195	WKRQQLAKNLGILPMLITYAGTRILIR-RPSTERKRAVLRLFTIMIVYFLWTA 253	R; Combodiere, C.; Ahuja, S. K.; Murphy, P. M.
Qy	250	PNTVLLNTEQFPGLNCCSSNNRLDAMQVETLGMTHCCINPILYAFVGKEFRNYLL 309	J. Biol. Chem. 270, 16491-16494, 1995
Db	*	254 PYNDVSVPQAFQDVFPTNOEQSKHLDLAMQVETLGMTHCCINPILYAFVGKEFRNYLL 313	A; Title: Cloning and functional expression of a human eosinophil CC chemokine receptor. A; Reference number: A57237; MUID: 95348056; PMID: 7622448
Qy	310	VFFQKHIAKRFCKCSCISQEAPERASSTGVTSRGEQSISVG 351	A; Status: nucleic acid sequence not shown
Db	*	314 QLFQRHVIALPLAKWLPPLSVQDLERTSST-SPSTGEHNL-SAG 354	A; Residues: 1-106; 'N', 108-275, 'S', 277-280, 'R', 282-355 <COM>
Qy			A; Cross-references: GB:U28694; NID:gi199579; PID:gi50469.1; PID:9119580
Db			A; Note: the translated sequence in GenBank entry HSU28694, release 113.0, PIDN: AAC50469
			C; Genetics:
			A; Gene: GDB: CMKB3
			A; Cross-references: GDB: 579624; OMIM: 601268
			A; Map position: 3p21-3p21
			C; Superfamily: vertebrate rhodopsin
			C; Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
			C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
			C; Accession: I49341
			A; Title: Cloning and differential tissue-specific expression of three mouse beta chemokines. J. Biol. Chem. 270, 1794-17501, 1995
			A; Reference number: I49339; MUID: 95340546; PMID: 7542241
			A; Accession: I49341
			A; Status: preliminary; translated from GB/EMBL/DBJ
			A; Molecule type: DNA
			A; Residues: 1-359 <RES>
			A; Cross-references: UNIPROT:Q8K3M7; EMBL:U28406; PID:9881551; PID:9881552
			C; Superfamily: vertebrate rhodopsin
			Query Match 50.9%; Score 936.5; DB 2; Length 355;
			Best Local Similarity 53.0%; Pred. No. 2, 8e-69;
			Matches 176; Conservative 64; Mismatches 89; Indels 3; Gaps 3;
Qy	20	COKINVQIAARILPPLSLVPTFGFVNMLVTLILNCRKLSMTDIYLNLIAISDLFF 79	Query Match 50.9%; Score 936.5; DB 2; Length 355;
Db	24	CIEADTRALMAQFPVPLPSLVTVGLGNVVVMILKYRRRIMTINYLNIAISDLFF 83	Best Local Similarity 53.0%; Pred. No. 2, 8e-69;
			Matches 176; Conservative 64; Mismatches 89; Indels 3; Gaps 3;
Qy	80	LITTPFWAHYLLA-QMDRGNTMQLLIGLYFEGSIFPFILITIDRYLAIVHAYFALK 138	Query Match 50.9%; Score 936.5; DB 2; Length 355;
Db	84	LVTLPFWTHYVRCHEHNFEGHGMCKLSCSFYHTGLYSEEFFIILITIDRYLAIVHAYFALK 143	Best Local Similarity 53.0%; Pred. No. 2, 8e-69;
			Matches 176; Conservative 64; Mismatches 89; Indels 3; Gaps 3;
Qy	139	ARTTFGVVTSVTVWWAVFASLDPGIIIFTRSGKEGLYTCSSHFVPSQYQFWPKI 198	Query Match 50.9%; Score 936.5; DB 2; Length 355;
Db	144	ARTTFGVVTSVTVWGAVLAALPEFYETEELFEETLCSALVYPEDTVSYRHFHTIRM 203	Best Local Similarity 53.0%; Pred. No. 2, 8e-69;
			Matches 176; Conservative 64; Mismatches 89; Indels 3; Gaps 3;
Qy	199	VLGLVLPILMVYCYSGLKTLLRCNEKKRRAVLIFTIMIVYFLWAPYIVNLIN 258	Query Match 50.9%; Score 936.5; DB 2; Length 355;
Db	204	TIPFLVLLWMAICYTGKIKLRLCPs-KKKYKAIIFVITMAVFFIFWTPIVNAVLL 262	Best Local Similarity 53.0%; Pred. No. 2, 8e-69;
			Matches 176; Conservative 64; Mismatches 89; Indels 3; Gaps 3;
Qy	259	TQEQFFGLNCSSNSNRDOAMQVETLGMTHCCINPILYAFVGKEFRNYLLVFFQKHTAK 318	Query Match 50.9%; Score 936.5; DB 2; Length 355;
Db	263	SYDSLFGNDCERTKHLDDLMVLYTEVAYSHCCMNVPYAFGERFRKYLRFHRHLLM 322	Best Local Similarity 53.0%; Pred. No. 2, 8e-69;
			Matches 176; Conservative 64; Mismatches 89; Indels 3; Gaps 3;
Qy	319	RFCCKCSIPQQEAPERASSVYTRSTGEBISV 350	Query Match 50.9%; Score 936.5; DB 2; Length 355;
Db	323	HGRYIPFLPSEKLERISSV-SPSTAPELSI 353	Best Local Similarity 53.0%; Pred. No. 2, 8e-69;
			Matches 176; Conservative 64; Mismatches 89; Indels 3; Gaps 3;
Qy	321	HRVQFTWENIFQFLPGEENGRTSSV-SFSTGEQEBISV 357	Query Match 50.9%; Score 936.5; DB 2; Length 355;
Db			Best Local Similarity 53.0%; Pred. No. 2, 8e-69;
			Matches 176; Conservative 64; Mismatches 89; Indels 3; Gaps 3;
Qy	37	RESULT 8	Result 8
Db	57160	chemokine (C-C) receptor 4 - human	A57160
		N; Alternative names: C-C CKR-4	
		C; Species: Homo sapiens (man)	
		C; Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004	
		C; Accession: A57160	
		R; Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K. B.; Hoogewerf, A.J.; Proudfoot, A.R.I.; ;	
		J. Biol. Chem. 270, 19495-19500, 1995	
		A; Title: Molecular cloning and functional expression of a novel CC chemokine receptor cI	
		R; Ponath, P.D.	
		Submitted to the EMBL Data Library, February 1996	
		A; Reference number: H01272	
		A; Accession: G02436	
		A; Status: translated from GB/EMBL/DBJ	
		A; Molecule type: DNA	
		A; Residues: 1-355 <PON>	
		A; Cross-references: UNIPROT: P51679; GB:X85740; NID:91370103; PIDN: AAC59743.1; PID: 99714.	
		A; Note: source clone K5-5	

C;Genetics:							
A;Gene: GDB:CMKBR4	49.6%	Pred. No. 2.3e-66;	Mismatches 98;	Indels 6;	Gaps 4;		
A;Cross-references: GDB:677463							
C;Superfamily: vertebrate rhodopsin							
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein							
F;40-65/Domain: transmembrane #status predicted <TM1>							
F;112-133/Domain: transmembrane #status predicted <TM2>							
F;151-175/Domain: transmembrane #status Predicted <TM3>							
F;208-226/Domain: transmembrane #status Predicted <TM4>							
F;243-264/Domain: transmembrane #status Predicted <TM5>							
F;291-308/Domain: transmembrane #status Predicted <TM6>							
F;29-276,110-187/Disulfide bonds: #status predicted							
F;72,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted							
F;183,194/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted							
F;321/Binding site: carbohydrate (Asn) (covalent) (by protein kinase C) #status predicted							
Query Match 49.6%; Score 914; DB 2; Length 360;							
Best Local Similarity 49.6%; Pred. No. 2e-67;							
Matches 175; Conservative 65; Mismatches 100; Indels 10; Gaps 6;							
Db 8 DTLDIESYS-NVLYESIIPKPCTKEGIAKGELFLPPLPLSVEFGNLGNSSVVLVLFK 66							
Qy 58 CKRLKSMTDYLINNIAISDIFLFLTYPFWAHYLLAQWDFANTMCLLGLYFGEFFSGIF 117							RESULT 10
Db 67 YKLRSMTDYLINNIAISDIFLFLTYPFWAHYLLAQWDFANTMCLLGLCMISSWLYCFYSGF 126							S55594
Qy 118 FIIILTDIYLAVHAWFALKARTVTFGVTSITWVAVFASLPGIITFRSQEGLMYT 177							G protein-coupled receptor E1 - equine herpesvirus 2
Db 127 FVMLMSIDTYLAIHVAFSLRARTLTGVITSATWSVAFASLPGIIFSTCYTERNTY 186							C;Species: equine herpesvirus 2
Qy 178 CSSHPAPSYQOFWKNFQTLKIVIGLGLVLPILVWTCYSGILKTLLRCNEKKHRAYVLL 237							C;Accession: S55594
Db 187 CKTKYSLNS-TTWKVLISLEINILGLVUPIGIMLFCYSMIRILQHCKNEKK-NKAIVMI 244							R;Pelford, B.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
Qy 238 FTIMIVYFLWAFNIVLILINTOFFGFLNCSSSNRQAMQYETETGMTHCCINPIYY 297							J. Mol. Biol. 249: 520-528, 1995
Db 245 FAVVFLFGFWTPNIVLFLFLETLEVQDCTPERYLIAQATETIAFVHCCLNPIYY 304							A;Title: The DNA sequence of equine herpesvirus 2.
Qy 298 AFVGKPKRNLYLVFFQKHIAKRF - CKCCSIFQQEAPERSYYTRSGEQEI 348							A;Reference number: S55594; PMID:9530501; PMID:7783207
Db 305 FFLGKFKRYVILQLF-KTCRGLFVLCQYCLLQIYSAOTPSSSYTQSTMHDHL 356							A;Status: preliminary; nucleic acid sequence not shown
Query Match 45.2%; Score 832; DB 2; Length 383;							A;Molecule type: DNA
Best Local Similarity 47.4%; Pred. No. 1.1e-60;							A;Residues: 1-383 <TEL>
Matches 157; Conservative 65; Mismatches 101; Indels 8; Gaps 3;							C;Cross references: UNIPROT:Q89609; GB:U20824; PIDN:9695172; PID:969517
Db 53 DVDTESSAPCYSDTTRLAQVTPALYLVLFGLGNLWVIVIRYMKNLTNMLL 112							C;Superfamily: vertebrate rhodopsin
Qy 71 NLAISDIFLFLTYPFWAHYLLAQWDFANTMCLLGLYFGEFFSGIFFIITIDRYL 128							C;Keywords: G protein-coupled receptor
Db 113 NLAISDIFLFLTYPFWAHYLLAQWDFANTMCLLGLYFGEFFSGIFFIITIDRYL 172							Query Match 45.2%; Score 832; DB 2; Length 383;
Qy 129 AVVHAWFALKARTVTFGVTSITWVAVFASLPGIITFRSQEGLHYTCSSHFPPSQYQ 188							Best Local Similarity 47.4%; Pred. No. 1.1e-60;
Db 173 AVVYAVTALRFPFTVTCGIVTCVCTWFLAGLSSIEPFPHGHQODNGRVQCDPYPENSTN 232							Matches 157; Conservative 65; Mismatches 101; Indels 8; Gaps 3;
Qy 189 FWKNFQTLKIVIGLGLVLPILVWTCYSGILKTLLRCNEKKHRAYVLLFTIMIVYFLW 248							Db 53 DVDTESSAPCYSDTTRLAQVTPALYLVLFGLGNLWVIVIRYMKNLTNMLL 112
Db 233 VWRHAYAKVIMSLPLIMAVCYVIIIRRLL-REPSKKYKAIJLIVMVAYFW 291							Qy 71 NLAISDIFLFLTYPFWAHYLLAQWDFANTMCLLGLYFGEFFSGIFFIITIDRYL 128
Qy 249 APYNIVLILNTQEFGLNNCSSLRDOAMQYETETGMTHCCINPIYYAFGEKERNYL 308							Db 292 TPVNIVLILSTPFTANLQCAALSNUDMALLJITKVAYTHCCINPVUYAFGEKFRBL 351
Db 292 TPVNIVLILSTPFTANLQCAALSNUDMALLJITKVAYTHCCINPVUYAFGEKFRBL 351							Qy 309 LVPFQKHIAKRFCKCSIFEQ----QEPAPER 334
Qy 352 YHRPHTYVAYLCKYIPLSGDGEKGKGPTR 382							Db 352 YHRPHTYVAYLCKYIPLSGDGEKGKGPTR 382
Query Match 48.9%; Score 901; DB 2; Length 360;							

Db	4 SFPELDIENPEYDDSAEACTYLGVGDIVAFGTLSIVFSLVFTGLVGNNLLVLTNSRKS	63	Db	138 MNRTTYQHGYTISLGWAAAILVAAAPQFMETK-OKEN-- ECLGDYPEVQEIWPVLRNV 193
Qy	62 KSMTDIYLNLTAISD1LFFLITYPEFWAHYLAQAWDFENTMCOLLTCIYFGFFSGIFFIIL 121	Db	197 KIVLIGLVLPLLVNVVYCYSGILKTKLRCNEKKHRAYRLIFTIMIVYFLWADPYNIVLJ 256	
Db	64 KSMTDIYLNLTAISD1LFFLITYPEFWAHYLAQAWDFENTMCOLLTCIYFGFFSGIFFIIL 123	Qy	198 BTNNFGFLPDLINNSCYPRIQTLPSCKRNHKKA-KAIKLILLVIVFFFPLWTPVNVMIF 252	
Qy	122 LTIDRYLVAVYHAVALKARTTGFVTTGVTTSVITWWVAVFASLPGIITRSOKEGLYHTCSHH 181	Db	257 LNTFOEFFGLNNCSSLSSNRDQAMQVETELGMTHCCINPIIYAFGKFRNYLLVFQKHI 316	
Db	124 ISIDRYLVAIILAANSNNRVTQHGVTISLGWAAAILVAAAPQFMETKRDN---ECLGD 179	Qy	258 LETKLKYDPPSCMRKDURLASSTETVAFSHCCLNPJUYAFGEKFRBLVLYGKCL 312	
Qy	182 PPYSQVFWKNFQTLKIVIGLVLVPMVTCYSGILKTLRCRNEKKHRAYRLIFTIM 241	Db	259 LETKLKYDPPSCMRKDURLASSTETVAFSHCCLNPJUYAFGEKFRBLVLYGKCL 312	
Db	180 YPEVLOEIPWPLERSEVNILGVLPLIMSPCYFRIVTLPSCKRKKA-RAIRLILVV 238	Qy	317 A 317	
Qy	242 IVYFLFWAPNIVLINTFQDEFFGLNNCSSLSSNRDQAMQVETELGMTHCCINPIIYAFG 301	Db	313 A 313	
Db	239 VVFFLFWTPNIVIPLTFLKYNFPPSCGMKRDLRWAISVETVAFSHCCLNPJUYAFG 298	RESULT 15		
Qy	302 EKERNYLLVFQKHIAKRFCKCCSF------ QEAPEPRASSVYTRSTGQBI 348	Db	JCS542 Chemokine receptor - human	
Db	299 EKFRRYL-----RHU--YNKCLAVLGRCYHAGFSTESRSRDSLSSLTHYTSESEG 350	Qy	C;Species: Homo sapiens (man)	
Qy	349 SV 350	Db	C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004	
Db	351 SL 352	Qy	C;Accession: JCS542	
Qy	36.4% Score 670; DB 2; Length 344;	Db	R;Fan, P.; Kyaw, H.; Su, K.; Zeng, Z.; Augustus, M.; Carter, K.C.; Li, Y.	
Qy	Best Local Similarity 40.9%; Pred. No. 1.7e-47;	Db	A;Title: Biophys. Res. Characterization of a novel human chemokine receptor.	
Qy	Matches 137; Conservative 64; Mismatches 108; Indels 7;	Db	A;Reference number: JCS542; PMID:9473515	
Qy	Query Match 36.4%; Score 670; DB 2; Length 344;	Db	A;Accession: JCS542	
Qy	Best Local Similarity 40.9%; Pred. No. 1.7e-47;	Db	A;Molecule type: DNA	
Qy	Matches 137; Conservative 64; Mismatches 108; Indels 7;	Db	A;Cross-references: UNIPROT:O00421; GB:U97123; NID:92897070; PID:92897	
Qy	Query Match 36.4%; Score 670; DB 2; Length 344;	Db	C;Superfamily: vertebrate rhodopsin	
Qy	Best Local Similarity 40.9%; Pred. No. 1.7e-47;	Db	A;Status: preliminary	
Qy	Matches 137; Conservative 64; Mismatches 108; Indels 7;	Db	A;Residues: 1-344 <FAN>	
Qy	Query Match 36.4%; Score 670; DB 2; Length 344;	Db	A;Cross-references: 1-344 <FAN>	
Qy	Best Local Similarity 40.9%; Pred. No. 1.7e-47;	Db	A;Superfamily: vertebrate rhodopsin	
Qy	77 LFPLLTVPWAHYLAQNDFGNTMCQLLTGPFLPLVPIFGVGNNMVLILLINCGRKSMTDIVLNLAI SD 135	Db	Qy 17 SEPCOKINYKQIAARLLPPLYSVLPFIFGFGVGNNMVLILLINCGRKSMTDIVLNLAI SD 76	
Qy	85 LCFLPTLIPFAH-----AGGDPMKLQALSPVLSQVPLCASFVQVGLDNLVLVLYKVKOLKRVNIVLNLAVN 138	Db	Db 25 AEQCDKDYDQALSPVLSQVPLCASFVQVGLDNLVLVLYKVKOLKRVNIVLNLAVN 84	
Qy	136 ALKARTVTFGVVTSVITAVVAVFASLPGIITRSQKEGHLYHTCS-SHFYY-SOYQFWQN 192	Qy	Qy 77 LFPLLTVPWAHYLAQNDFGNTMCQLLTGPFLPLVPIFGVGNNMVLILLINCGRKSMTDIVLNLAI SD 135	
Qy	139 FSARRRVPGGITISVLAWTAILATLPEVYVYKQMBDKYKCAFSPRPFLPADETFWKH 198	Db	Db 25 LCFLPTLIPFAH-----AGGDPMKLQALSPVLSQVPLCASFVQVGLDNLVLVLYKVKOLKRVNIVLNLAVN 138	
Qy	193 FQTLKIVLGLVPLVNVVICSGILKTLLRCNEKKHRAYRLIFTIMIVYFLWAPYN 252	Qy	Db 136 ALKARTVTFGVVTSVITAVVAVFASLPGIITRSQKEGHLYHTCS-SHFYY-SOYQFWQN 192	
Qy	199 FLTLMKNTSVLVPLFLIFTFLYQMRKTL--RFREQYSLFQLVFMVFLMWAPYN 255	Db	Db 139 FSARRRVPGGITISVLAWTAILATLPEVYVYKQMBDKYKCAFSPRPFLPADETFWKH 198	
Qy	253 IVLLINTFOEFFGLNNCSSLSSNRDQAMQVETELGMTHCCINPIIYAFGKFRNYLLVF 312	Qy	Db 193 FQTLKIVLGLVPLVNVVICSGILKTLLRCNEKKHRAYRLIFTIMIVYFLWAPYN 252	
Qy	256 IAPPPLSTPKHEFSISDCESSYNLDKSVHITKLIAITHCCINPLLYAFLDGTPSKYL--- 311	Db	Db 199 FLTLMKNTSVLVPLFLIFTFLYQMRKTL--RFREQYSLFQLVFMVFLMWAPYN 255	
Qy	313 QKRIAKRPFKCCSTFOQQAPEARSVYTRSTGQE 347	Qy	Qy 253 IVLLINTFOEFFGLNNCSSLSSNRDQAMQVETELGMTHCCINPIIYAFGKFRNYLLVF 312	
Qy	312 -----CRCFHL-RSNTPLQPRGQSQGQTSTSREB 337	Db	Db 256 IAPPPLSTPKHEFSISDCESSYNLDKSVHITKLIAITHCCINPLLYAFLDGTPSKYL--- 311	
Qy	Search completed: October 3, 2005, 07:48:34	Qy	Qy 313 QKRIAKRPFKCCSTFOQQAPEARSVYTRSTGQE 347	
Qy	Job time : 29 secs	Qy	Qy 312 -----CRCFHL-RSNTPLQPRGQSQGQTSTSREB 337	
Qy	17 SEPCOKINYKQIAARLLPPLYSVLPFIFGFGVGNNMVLILLINCGRKSMTDIVLNLAI SD 76	Qy	Qy 312 -----CRCFHL-RSNTPLQPRGQSQGQTSTSREB 337	
Db	18 AEACTYDIDVFPWTHYLINEKGJLHNAMCKFTTAFFGFFSGIFFIILTDRYLAHVWPA 136	Db	Qy 17 SEPCOKINYKQIAARLLPPLYSVLPFIFGFGVGNNMVLILLINCGRKSMTDIVLNLAI SD 76	
Qy	77 LFPLLTVPWAHYLAQNDFGNTMCQLLTGPFLPLVPIFGVGNNMVLILLINCGRKSMTDIVLNLAI SD 77	Db	Db 18 AEACTYDIDVFPWTHYLINEKGJLHNAMCKFTTAFFGFFSGIFFIILTDRYLAHVWPA 136	
Db	78 LLFVATLPPMTHYLINEKGJLHNAMCKFTTAFFGFFSGIFFIILTDRYLAHVWPA 137	Qy	Qy 77 LFPLLTVPWAHYLAQNDFGNTMCQLLTGPFLPLVPIFGVGNNMVLILLINCGRKSMTDIVLNLAI SD 77	
Qy	137 LKARTVTFGVVTSVITWWVAVFASLPGIITRSOKEGLYHTCSHHFPPSQYQFWQNFRTL 196	Db	Db 78 LLFVATLPPMTHYLINEKGJLHNAMCKFTTAFFGFFSGIFFIILTDRYLAHVWPA 137	

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 3, 2005, 06:53:54 ; Search time 98 Seconds
1839.305 Million cell updates/sec
(without alignments)

Title: US-10-700-313-2
Perfect score: 1841

Sequence: 1 MDYQVSSPIYDINYTTSEPC.....BRASSVYTRSTGBQEISVGL 352

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : UniProt 03:
1: uniprot_sprot:
2: uniprot_trembl:
*

RESULT 1

CKR5_HUMAN

STANDARD

PRP;

352 AA.

ID P51681; O14693; O14697; O14698;

AC O14701; O14702; O14703; O14705; O14706; O14707;

AC O14708; O15588; Q9UPA4;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DB C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5)

(HIV-1 fusion coreceptor) (CHEMR13) (CD195 antigen).

GN Name=CCB5; Synonyms=CMKRS;

OS Homo sapiens (Human).

EBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX Sambon M., Labbe O., Mollerseau C., Vassart G., Parmentier M.:

RT "Molecular cloning and functional expression of a new human CC-

RT chemokine receptor gene.";

RL Biochemistry 35:3362-3367(1996).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=96291862; PubMed=8663314; DOI=10.1074/jbc.271.29.17161;

RA Raport C.J., Gosling J., Schweichart V.L., Gray P.W., Charo I.F.;

RT "Molecular cloning and functional characterization of a novel human CC

RT chemokine receptor (CCR5) for RANTES, MIP-1 β , and MIP-1 α ."

RL J. Biol. Chem. 271:17161-17166(1996).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=96295970; PubMed=8699119;

RA Combadiere C., Ahuja S.K., Tiffany H.L., Murphy P.M.;

RA Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,

RA Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,

RA Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,

RA Dragan Y., Giacalone J., Pie A., Powell E., Solinsky K.A., Desilva U.,

RA Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,

RA Sacripanti J.L.;

RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RX McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,

RA Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,

RA Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,

RA Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,

RA Dragan Y., Giacalone J., Pie A., Powell E., Solinsky K.A., Desilva U.,

RA Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,

RA Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.

ALIGNMENTS

32	1808	98.2	352	2	097962 Pygathrix a
33	1808	98.2	352	2	Q71zz7 macaca nigr
34	1808	98.2	352	2	Q71zz8 macaca tonk
35	1808	98.2	352	2	Q71zz9 macaca sin
36	1808	98.2	352	2	Q7ij34 Pygathrix r
37	1807	98.2	352	2	Q95nc1 theropithec
38	1807	98.2	352	2	Q9xt14 colobus gue
39	1806	98.1	352	2	Q95nc3 molopithec
40	1806	98.1	352	2	Q95nc6 trachypithe
41	1804	98.0	352	2	Q9xt13 papiro anub
42	1803	97.9	352	2	Q18770 pan troglod
43	1803	97.9	352	2	Q9t870 cercopithec
44	1803	97.9	352	2	Q9tv49 cercocebus
45	1802	97.9	352	2	Q97975 macaca arct

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1836	99.7	352	1	P51681 homo sapien
2	1830	99.4	352	1	P60574 pan paniscus
3	1830	99.4	352	1	P56440 pan troglod
4	1825	99.1	352	1	P61756 pongo pygma
5	1825	99.1	352	1	07981 pongo pygma
6	1825	99.1	352	2	Q71tz2 pongo pygma
7	1820	98.9	352	1	P56439 gorilla gorilla
8	1820	98.9	352	1	Q95nc5 hylobates s
9	1820	98.9	352	2	Q71tz0 gorilla gorilla
10	1820	98.9	352	2	Q71tz1 gorilla gorilla
11	1818	98.8	352	2	Q18771 pan troglod
12	1818	98.8	352	2	Q18772 pan troglod
13	1817	98.7	352	2	Q9xs99 gorilla gorilla
14	1816	98.6	352	1	P61757 semnopithec
15	1816	98.6	352	1	Q97979 trachypithe
16	1816	98.6	352	2	Q71tz6 trachypithe
17	1813	98.6	352	2	Q9tv50 pan troglod
18	1813	98.5	352	1	Q95nc0 hylobates m
19	1812	98.4	352	2	Q95nc7 nasalis lar
20	1811	98.4	352	1	P61755 lophocebus
21	1811	98.4	352	1	P62629 papio anubis
22	1811	98.4	352	1	P63270 papio hamadryas
23	1811	98.4	352	1	Q97878 trachypithe
24	1811	98.4	352	2	Q9nc8 colobus poli
25	1811	98.4	352	2	Q71ui8 cercopithec
26	1810	98.3	352	1	Q97880 pygathrix b
27	1810	98.3	352	1	Q97882 pygathrix n
28	1809	98.3	352	1	C9K5_HYL1
29	1808	98.2	352	1	C9K5_MACU
30	1808	98.2	352	1	C9K5_MACMU
31	1808	98.2	352	1	C9K5_MACNE

SEQUENCE FROM N.A.

RX PMID=98001387; PubMed=9343222;

RA Kubmann S.E., Platt E.J., Kozak S.L., Kabat D.;

RT "Polymorphisms of the CCR5 genes of African green monkeys and mice implicate specific amino acids in infections by simian and human

FT	TRANSMEM DOMAIN	69	89	2 (Potential).	
		90	102	Extracellular (Potential).	
Query Match	Score 1836; DB 1; Length 352;				
Best Local Similarity 99.7%; Pred. No. 4.2e-105;					
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
Qy	1 MDYQSSPIYDINYTTSPCQKINVQIAARLLPPISLYVPIFGFWGNYMLVILLINCKR 60				
Db	1 MDYQSSPIYDINYTTSPCQKINVQIAARLLPPISLYVPIFGFWGNYMLVILLINCKR 60				
Qy	61 LKSMTDYLNLAIISDIFELLTVPFAHYLAQWDDEGNTMQLGLYPTGFSGTIPFII 120				
Db	61 LKSMTDYLNLAIISDIFELLTVPFAHYAAQWDDEGNTMQLGLYPTGFSGTIPFII 120				
Qy	121 LLTIDYLAVVHAFLAKARTVTFGTTSVITWVVAVASLPGIPTPSREGEGLHYTCSS 180				
Db	121 LLTIDYLAVVHAFLAKARTVTFGTTSVITWVVAVASLPGIPTPSREGEGLHYTCSS 180				
Qy	181 HFPYSQYQFWKNFQTLKIVILGLVLPLUVWVYCSSLKLTKLRCNEKGRHARVLIFTI 240				
Db	181 HFPYSQYQFWKNFQTLKIVILGLVLPLUVWVYCSSLKLTKLRCNEKGRHARVLIFTI 240				
Qy	241 MIVYFLWAPWPNTIVLLINTPQFFGUNCCSNTQFQEAPEASSVYTRSTGEQEVSVGL 352				
Db	241 MIVYFLWAPWPNTIVLLINTPQFFGUNCCSNTQFQEAPEASSVYTRSTGEQEVSVGL 352				
Qy	301 GEKFRTNLLVFQPKHIAKRFCKCCS1FQQEAPEASSVYTRSTGEQEVSVGL 352				
Db	301 GEKFRTNLLVFQPKHIAKRFCKCCS1FQQEAPEASSVYTRSTGEQEVSVGL 352				
<hr/>					
RESULT 2					
ID	CKR5_PANPA	STANDARD;	PRT;	352 AA.	
AC	P60574;				
DT	29-MAR-2004 (Rel. 43, Created)				
DT	29-MAR-2004 (Rel. 43, Last sequence update)				
DT	25-OCT-2004 (Rel. 45, Last annotation update)				
DE	C-C chemokine receptor type 5 (C-C CKR-5) (CCR5).				
GN	Name=CKR5; Synonyms=CMKBR5;				
OS	Pan paniscus (Pygmy chimpanzee) (Bonobo).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.				
OX	NCBI_TaxID:9597;				
RN	SEQUENCE FROM N.A.				
RA	Zhang Y., Ryder O.A., Zhang Y.;				
RT	"Sequence comparison of the CCR5 gene in primates and primate phylogeny.";				
RL	Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.				
CC	-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-beta and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or differentiation.				
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.				
CC	-!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; AP177893; AAK43376.1; -.				
DR	Pfam; PF00001; Tm1; 1.				
DR	PRINTS; PR00237; GPCRRODOPSN.				
DR	PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.				
DR	PROSITE; PS05262; G-PROTEIN_REC_EP_F1_2; 1.				
KW	G-protein coupled receptor; Glycoprotein; Sulfation; Transmembrane simian immunodeficiency virus strains".;				
RP	SEQUENCE FROM N.A.				
RA	MEDLINE=9726687; PubMed=9108095; DOI=10.1073/pnas.94.8.4005;				
RA	Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,				
RA	Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,				
RA	Peppe S.C., Parmentier M., Broder C.C., Doms R.W.;				
RT	"Differential utilization of CCR5 by macrophage and T cell tropic simian immunodeficiency virus strains".;				

Qy	241	MIVYFLWAPYNIVLNLNTQEFFGLNCSSSNRLDQAMQVTETLGMTCCINPITYAFV	300	
Db	241	MIVYFLWAPYNIVLNLNTQEFFGLNCSSSNRLDQAMQVTETLGMTCCINPITYAFV	300	
Qy	301	GEKFRNYLLVFQKRHKRCKCCSIFQQEAPERASSYYTRSTGQEISVGL	352	
Db	301	GEKFRNYLLVFQKRHKRCKCCSIFQQEAPERASSYYTRSTGQEISVGL	352	
		RESULT 6		
Q71T22		PRELIMINARY;	PRT;	352 AA.
AC	Q71T22;			
DT	05-JUL-2004	(TREMBUREL. 27, Created)		
DT	05-JUL-2004	(TREMBUREL. 27, Last sequence update)		
DT	05-JUL-2004	(TREMBUREL. 27, Last annotation update)		
DE		C-C chemokine receptor 5.		
GN	Name=CCR5; Synonyms=CMKBR5;			
OS	Pongo pygmaeus (Bornean orangutan).			
OC	Mammalia; Eutheria; Chordata; Craniata; Buteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.			
NCBI_TaxID	9602;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Zhang Y.; Ryder O.A.; Zhang Y.;			
CC	Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.			
CC	- - SUBCELLULAR LOCATION: Integral membrane protein (By similarity).			
CC	- - SIMILARITY: Belongs to family 1 of G-protein coupled receptors.			
DR	EMBL: AF17900;			
DR	GO; GO:0016021;			
DR	GO; GO:0016493;			
DR	F: C-C chemokine receptor activity; IEA.			
DR	GO; GO:0004872;			
DR	F: Receptor activity; IEA.			
DR	GO; GO:0001584;			
DR	F: Rhodopsin like receptor activity; IEA.			
DR	GO; GO:0007186;			
DR	F: G-protein coupled receptor protein signalin. . ; IEA.			
DR	InterPro; IPR002240;			
DR	CC 5 receptor.			
DR	InterPro; IPR003355;			
DR	Chmkine receptor.			
DR	InterPro; IPR002276;			
DR	GPCR_Rhodpsn.			
DR	PFam; PF00001; 7tm_1; 1.			
DR	PRINTS; PR00567; CCHEMOKINER.			
DR	PRINTS; PR01110; CHEMOKINERS.			
DR	PROSITE; PS00237; G PROTEIN RECEPTOR.			
DR	PROSITE; PS00237; G PROTEIN RECEPTOR.			
DR	PROSITE; PS5046;			
KW	G-protein coupled receptor; Receptor; Transmembrane.			
SEQ	352 AA; F452F47135A658A CRC64;			
Query Match	99.1% Score 1825; DB 2; Length 352;			
Best Local Similarity	98.9% Pred. No. 2e-104;			
Matches 348; Conservative 2; Mismatches 2; Indels 0; Gaps 0;				
Qy	1 MDYQVSSPTYDINYNTSEPCQKTNQKIAARIPLPLYSVLFEGVNMLVILTLINKR	60		
Db	1 MDYQVSSPTYDINYNTSEPCQKTNQKIAARIPLPLYSVLFEGVNMLVILTLINKR	60		
Qy	61 LKSMTDIYLINLAISDLFFLTTPWAHHLAQADFGNTMCQLITGLYFIGPGSGIPII	120		
Db	61 LKSMTDIYLINLAISDLFFLTTPWAHHLAQADFGNTMCQLITGLYFIGPGSGIPII	120		
Qy	181 HFPYSQQFWKNFQTLKIVLVLPLVMVICSYGSLIKTLLCRNEKTHRAVLIFTI	240		
Db	181 HFPYSQQFWKNFQTLKIVLVLPLVMVICSYGSLIKTLLCRNEKTHRAVLIFTI	240		
Qy	241 MIVYFLWAPYNIVLNLNTQEFFGLNCSSSNRLDQAMQVTETLGMTCCINPITYAFV	300		
Db	241 MIVYFLWAPYNIVLNLNTQEFFGLNCSSSNRLDQAMQVTETLGMTCCINPITYAFV	300		
Qy	301 GEKFRNYLLVFQKRHKRCKCCSIFQQEAPERASSYYTRSTGQEISVGL	352		
Db	301 GEKFRNYLLVFQKRHKRCKCCSIFQQEAPERASSYYTRSTGQEISVGL	352		

Query Match 98.9% Score 1820; DB 1; Length 352;

Best Local Similarity 98.6%; Pred. No. 4e-104;

Qy	1 MDYQVSSPTYDINYNTSEPCQKTNQKIAARIPLPLYSVLFEGVNMLVILTLINKR	60		
Db	1 MDYQVSSPTYDINYNTSEPCQKTNQKIAARIPLPLYSVLFEGVNMLVILTLINKR	60		
Qy	61 LKSMTDIYLINLAISDLFFLTTPWAHHLAQADFGNTMCQLITGLYFIGPGSGIPII	120		
Db	61 LKSMTDIYLINLAISDLFFLTTPWAHHLAQADFGNTMCQLITGLYFIGPGSGIPII	120		
Qy	181 HFPYSQQFWKNFQTLKIVLVLPLVMVICSYGSLIKTLLCRNEKTHRAVLIFTI	240		
Db	181 HFPYSQQFWKNFQTLKIVLVLPLVMVICSYGSLIKTLLCRNEKTHRAVLIFTI	240		
Qy	241 MIVYFLWAPYNIVLNLNTQEFFGLNCSSSNRLDQAMQVTETLGMTCCINPITYAFV	300		
Db	241 MIVYFLWAPYNIVLNLNTQEFFGLNCSSSNRLDQAMQVTETLGMTCCINPITYAFV	300		
Qy	301 GEKFRNYLLVFQKRHKRCKCCSIFQQEAPERASSYYTRSTGQEISVGL	352		
Db	301 GEKFRNYLLVFQKRHKRCKCCSIFQQEAPERASSYYTRSTGQEISVGL	352		

Qy	1 MDYQVSSPTYDINYNTSEPCQKTNQKIAARIPLPLYSVLFEGVNMLVILTLINKR	60		
Db	1 MDYQVSSPTYDINYNTSEPCQKTNQKIAARIPLPLYSVLFEGVNMLVILTLINKR	60		
Qy	61 LKSMTDIYLINLAISDLFFLTTPWAHHLAQADFGNTMCQLITGLYFIGPGSGIPII	120		
Db	61 LKSMTDIYLINLAISDLFFLTTPWAHHLAQADFGNTMCQLITGLYFIGPGSGIPII	120		
Qy	181 HFPYSQQFWKNFQTLKIVLVLPLVMVICSYGSLIKTLLCRNEKTHRAVLIFTI	240		
Db	181 HFPYSQQFWKNFQTLKIVLVLPLVMVICSYGSLIKTLLCRNEKTHRAVLIFTI	240		
Qy	241 MIVYFLWAPYNIVLNLNTQEFFGLNCSSSNRLDQAMQVTETLGMTCCINPITYAFV	300		
Db	241 MIVYFLWAPYNIVLNLNTQEFFGLNCSSSNRLDQAMQVTETLGMTCCINPITYAFV	300		
Qy	301 GEKFRNYLLVFQKRHKRCKCCSIFQQEAPERASSYYTRSTGQEISVGL	352		
Db	301 GEKFRNYLLVFQKRHKRCKCCSIFQQEAPERASSYYTRSTGQEISVGL	352		

Qy	1 MDYQVSSPTYDINYNTSEPCQKTNQKIAARIPLPLYSVLFEGVNMLVILTLINKR	60		
Db	1 MDYQVSSPTYDINYNTSEPCQKTNQKIAARIPLPLYSVLFEGVNMLVILTLINKR	60		
Qy	61 LKSMTDIYLINLAISDLFFLTTPWAHHLAQADFGNTMCQLITGLYFIGPGSGIPII	120		
Db	61 LKSMTDIYLINLAISDLFFLTTPWAHHLAQADFGNTMCQLITGLYFIGPGSGIPII	120		
Qy	181 HFPYSQQFWKNFQTLKIVLVLPLVMVICSYGSLIKTLLCRNEKTHRAVLIFTI	240		
Db	181 HFPYSQQFWKNFQTLKIVLVLPLVMVICSYGSLIKTLLCRNEKTHRAVLIFTI	240		
Qy	241 MIVYFLWAPYNIVLNLNTQEFFGLNCSSSNRLDQAMQVTETLGMTCCINPITYAFV	300		
Db	241 MIVYFLWAPYNIVLNLNTQEFFGLNCSSSNRLDQAMQVTETLGMTCCINPITYAFV	300		
Qy	301 GEKFRNYLLVFQKRHKRCKCCSIFQQEAPERASSYYTRSTGQEISVGL	352		
Db	301 GEKFRNYLLVFQKRHKRCKCCSIFQQEAPERASSYYTRSTGQEISVGL	352		

Qy	1 MDYQVSSPTYDINYNTSEPCQKTNQKIAARIPLPLYSVLFEGVNMLVILTLINKR	60		
Db	1 MDYQVSSPTYDINYNTSEPCQKTNQKIAARIPLPLYSVLFEGVNMLVILTLINKR	60		
Qy	61 LKSMTDIYLINLAISDLFFLTTPWAHHLAQADFGNTMCQLITGLYFIGPGSGIPII	120		
Db	61 LKSMTDIYLINLAISDLFFLTTPWAHHLAQADFGNTMCQLITGLYFIGPGSGIPII	120		
Qy	181 HFPYSQQFWKNFQTLKIVLVLPLVMVICSYGSLIKTLLCRNEKTHRAVLIFTI	240		
Db	181 HFPYSQQFWKNFQTLKIVLVLPLVMVICSYGSLIKTLLCRNEKTHRAVLIFTI	240		
Qy	241 MIVYFLWAPYNIVLNLNTQEFFGLNCSSSNRLDQAMQVTETLGMTCCINPITYAFV	300		
Db	241 MIVYFLWAPYNIVLNLNTQEFFGLNCSSSNRLDQAMQVTETLGMTCCINPITYAFV	300		
Qy	301 GEKFRNYLLVFQKRHKRCKCCSIFQQEAPERASSYYTRSTGQEISVGL	352		
Db	301 GEKFRNYLLVFQKRHKRCKCCSIFQQEAPERASSYYTRSTGQEISVGL	352		

Qy	1 MDYQVSSPTYDINYNTSEPCQKTNQKIAARIPLPLYSVLFEGVNMLVILTLINKR	60		
Db	1 MDYQVSSPTYDINYNTSEPCQKTNQKIAARIPLPLYSVLFEGVNMLVILTLINKR	60		
Qy	61 LKSMTDIYLINLAISDLFFLTTPWAHHLAQADFGNTMCQLITGLYFIGPGSGIPII	120		
Db	61 LKSMTDIYLINLAISDLFFLTTPWAHHLAQADFGNTMCQLITGLYFIGPGSGIPII	120		
Qy	181 HFPYSQQFWKNFQTLKIVLVLPLVMVICSYGSLIKTLLCRNEKTHRAVLIFTI	240		
Db	181 HFPYSQQFWKNFQTLKIVLVLPLVMVICSYGSLIKTLLCRNEKTHRAVLIFTI	240		
Qy	241 MIVYFLWAPYNIVLNLNTQEFFGLNCSSSNRLDQAMQVTETLGMTCCINPITYAFV	300		
Db	241 MIVYFLWAPYNIVLNLNTQEFFGLNCSSSNRLDQAMQVTETLGMTCCINPITYAFV	300		
Qy	301 GEKFRNYLLVFQKRHKRCKCCSIFQQEAPERASSYYTRSTGQEISVGL	352		
Db	301 GEKFRNYLLVFQKRHKRCKCCSIFQQEAPERASSYYTRSTGQEISVGL	352		

Qy	1 MDYQVSSPTYDINYNTSEPCQKTNQKIAARIPLPLYSVLFEGVNMLVILTLINKR	60		
Db	1 MDYQVSSPTYDINYNTSEPCQKTNQKIAARIPLPLYSVLFEGVNMLVILTLINKR	60		
Qy	61 LKSMTDIYLINLAISDLFFLTTPWAHHLAQADFGNTMCQLITGLYFIGPGSGIPII	120		
Db	61 LKSMTDIYLINLAISDLFFLTTPWAHHLAQADFGNTMCQLITGLYFIGPGSGIPII	120		
Qy	181 HFPYSQQFWKNFQTLKIVLVLPLVMVICSYGSLIKTLLCRNEKTHRAVLIFTI	240		
Db	181 HFPYSQQFWKNFQTLKIVLVLPLVMVICSYGSLIKTLLCRNEKTHRAVLIFTI	240		
Qy	241 MIVYFLWAPYNIVLNLNTQEFFGLNCSSSNRLDQAMQVTETLGMTCCINPITYAFV	300		
Db	241 MIVYFLWAPYNIVLNLNTQEFFGLNCSSSNRLDQAMQVTETLGMTCCINPITYAFV	300		
Qy	301 GEKFRNYLLVFQKRHKRCKCCSIFQQEAPERASSYYTRSTGQEISVGL	352		
Db	301 GEKFRNYLLVFQKRHKRCKCCSIFQQEAPERASSYYTRSTGQEISVGL	352		

Qy	1 MDYQVSSPTYDINYNTSEPCQKTNQKIAARIPLPLYSVLFEGVNMLVILTLINKR	60		
Db	1 MDYQVSSPTYDINYNTSEPCQKTNQKIAARIPLPLYSVLFEGVNMLVILTLINKR	60		
Qy	61 LKSMTDIYLINLAISDLFFLTTPWAHHLAQADFGNTMCQLITGLYFIGPGSGIPII	120		
Db	61 LKSMTDIYLINLAISDLFFLTTPWAHHLAQADFGNTMCQLITGLYFIGPGSGIPII	120		
Qy	181 HFPYSQQFWKNFQTLKIVLVLPLVMVICSYGSLIKTLLCRNEKTHRAVLIFTI	240		
Db	181 HFPYSQQFWKNFQTLKIVLVLPLVMVICSYGSLIKTLLCRNEKTHRAVLIFTI	240		
Qy	241 MIVYFLWAPYNIVLNLNTQEFFGLNCSSSNRLDQAMQVTETLGMTCCINPITYAFV	300		
Db	241 MIVYFLWAPYNIVLNLNTQEFFGLNCSSSNRLDQAMQVTETLGMTCCINPITYAFV	300		
Qy	301 GEKFRNYLLVFQKRHKRCKCCSIFQQEAPERASSYYTRSTGQEISVGL	352		
Db	301 GEKFRNYLLVFQKRHKRCKCCSIFQQEAPERASSYYTRSTGQEISVGL	352		

Qy	1 MDYQVSSPTYDINYNTSEPCQKTNQKIAARIPLPLYSVLFEGVNMLVILTLINKR	60		
Db	1 MDYQVSSPTYDINYNTSEPCQKTNQKIAARIPLPLYSVLFEGVNMLVILTLINKR	60		
Qy	61 LKSMTDIYLINLAISDLFFLTTPWAHHLAQADFGNTMCQLITGLYFIGPGSGIPII	120		
Db	61 LKSMTDIYLINLAISDLFFLTTPWAHHLAQADFGNTMCQLITGLYFIGPGSGIPII	120		
Qy	181 HFPYSQQFWKNFQTLKIVLVLPLVMVICSYGSLIKTLLCRNEKTHRAVLIFTI	240		
Db	181 HFPYSQQFWKNFQTLKIVLVLPLVMVICSYGSLIKTLLCRNEKTHRAVLIFTI	240		
Qy	241 MIVYFLWAPYNIVLNLNTQEFFGLNCSSSNRLDQAMQVTETLGMTCCINPITYAFV	300		
Db	241 MIVYFLWAPYNIVLNLNTQEFFGLNCSSSNRLDQAMQVTETLGMTCCINPITYAFV	300		
Qy	301 GEKFRNYLLVFQKRHKRCKCCSIFQQEAPERASSYYTRSTGQEISVGL	352		
Db	301 GEKFRNYLLVFQKRHKRCKCCSIFQQEAPERASSYYTRSTGQEISVGL	352		

Qy	1 MDYQVSSPTYDINYNTSEPCQKTNQKIAARIPLPLYSVLFEGVNMLVILTLINKR	60		
Db	1 MDYQVSSPTYDINYNTSEPCQKTNQKIAARIPLPLYSVLFEGVNMLVILTLINKR	60		
Qy	61 LKSMTDIYLINLAISDLFFLTTPWAHHLAQADFGNTMCQLITGLYFIGPGSGIPII	120		
Db	61 LKSMTDIYLINLAISDLFFLTTPWAHHLAQADFGNTMCQLITGLYFIGPGSGIPII	120		
Qy	181 HFPYSQQFWKNFQTLKIVLVLPLVMVICSYGSLIKTLLCRNEKTHRAVLIFTI	240		
Db	181 HFPYSQQFWKNFQTLKIVLVLPLVMVICSYGSLIKTLLCRNEKTHRAVLIFTI	240		
Qy	241 MIVYFLWAPYNIVLNLNTQEFFGLNCSSSNRLDQAMQVTETLGMTCCINPITYAFV	300		
Db	241 MIVYFLWAPYNIVLNLNTQEFF			

DR	PROSITE; PS00237; G PROTEIN RECEPTOR_F1_1;	1.
DR	PROSITE; PS00262; G PROTEIN COUPLED RECEPTOR; Receptor; Transmembrane;	
KW	G-protein coupled receptor; Receptor; Transmembrane;	
DR	SEQUENCE 352 AA; 40515 MW; D0E6FCB9FB5EAC84 CRC64;	
DR	PROSITE; PS00237; G PROTEIN RECEPTOR_F1_1;	1.
KW	G-protein coupled receptor; Receptor; Transmembrane;	
PRINTS	PR00001; 7tm_1;	1.
PRINTS	PR00657; CCHEMOKINER.	
PRINTS	PR01110; CHEMOKINERS.	
PRINTS	PR00237; GPRRHODOPSN.	
DR	PROSITE; PS00237; G PROTEIN RECEPTOR_F1_1;	1.
KW	G-protein coupled receptor; Receptor; Transmembrane;	
SEQUENCE 352 AA; 40515 MW; D0E6FCB9FB5EAC84 CRC64;		
Query Match 98.9%; Score 1820; DB 2; Length 352;		
Best Local Similarity 98.6%; Pred. No. 4e-104; 2; Mismatches 3; Indels 0; Gaps 0;		
Matches 347; Conservative 2; Mismatches 3; Indels 0; Gaps 0;		
QY 1 MDYQVSSPDIYNTTSEPCQTKVQIAARLLPPLYSVLFVGVMVLLILINCKR 60	QY	1 MDYQVSSPDIYNTTSEPCQTKVQIAARLLPPLYSVLFVGVMVLLILINCKR 60
Db 1 MDYQVSSPDIYNTTSEPCQTKVQIAARLLPPLYSVLFVGVMVLLILINCKR 60	Db	1 MDYQVSSPDIYNTTSEPCQTKVQIAARLLPPLYSVLFVGVMVLLILINCKR 60
QY 61 LKSMTDIYLNLNLASDLEFLITDPEWAKHLLAQDDEGNMCOLLGLYPIGFSGIFFI 120	QY	61 LKSMTDIYLNLNLASDLEFLITDPEWAKHLLAQDDEGNMCOLLGLYPIGFSGIFFI 120
Db 61 LKSMTDIYLNLNLASDLEFLITDPEWAKHLLAQDDEGNMCOLLGLYPIGFSGIFFI 120	Db	61 LKSMTDIYLNLNLASDLEFLITDPEWAKHLLAQDDEGNMCOLLGLYPIGFSGIFFI 120
QY 121 LLTIDRYLAIVHFAVFKARTVTFQEVVTSVITWVVAFAASLPGLIFTTSQKEGHYTCS 180	QY	121 LLTIDRYLAIVHFAVFKARTVTFQEVVTSVITWVVAFAASLPGLIFTTSQKEGHYTCS 180
Db 121 LLTIDRYLAIVHFAVFKARTVTFQEVVTSVITWVVAFAASLPGLIFTTSQKEGHYTCS 180	Db	121 LLTIDRYLAIVHFAVFKARTVTFQEVVTSVITWVVAFAASLPGLIFTTSQKEGHYTCS 180
QY 181 HFPYSQYQFWKFNQFOTLKIVVGLVPLWVVICGSIKLTLRCRNEKKRHRVLFTI 240	QY	181 HFPYSQYQFWKFNQFOTLKIVVGLVPLWVVICGSIKLTLRCRNEKKRHRVLFTI 240
Db 181 HFPYSQYQFWKFNQFOTLKIVVGLVPLWVVICGSIKLTLRCRNEKKRHRVLFTI 240	Db	181 HFPYSQYQFWKFNQFOTLKIVVGLVPLWVVICGSIKLTLRCRNEKKRHRVLFTI 240
QY 241 MIVYFLFWAPYNNVLLINTFOEFLNQCNSSSNRLDQAMQVTTLGTMHCCINPIIYAFV 300	QY	241 MIVYFLFWAPYNNVLLINTFOEFLNQCNSSSNRLDQAMQVTTLGTMHCCINPIIYAFV 300
Db 241 MIVYFLFWAPYNNVLLINTFOEFLNQCNSSSNRLDQAMQVTTLGTMHCCINPIIYAFV 300	Db	241 MIVYFLFWAPYNNVLLINTFOEFLNQCNSSSNRLDQAMQVTTLGTMHCCINPIIYAFV 300
RESULT 11		
ID 018771 PRELIMINARY; PRT; 352 AA.	ID 018771 PRELIMINARY; PRT; 352 AA.	
AC 018771	AC 018771	
DT 01-JAN-1998 (TrEMBLref)	DT 01-JAN-1998 (TrEMBLref)	05 Created
DB 301 GEKFANYLLVVFQKHIAKRFKCCSIFQOEAPERASSYTRSTGEQELSVGL 352	DB 301 GEKFANYLLVVFQKHIAKRFKCCSIFQOEAPERASSYTRSTGEQELSVGL 352	
QY 301 GEKFANYLLVVFQKHIAKRFKCCSIFQOEAPERASSYTRSTGEQELSVGL 352	QY 301 GEKFANYLLVVFQKHIAKRFKCCSIFQOEAPERASSYTRSTGEQELSVGL 352	
Db 301 GEKFANYLLVVFQKHIAKRFKCCSIFQOEAPERASSYTRSTGEQELSVGL 352	Db 301 GEKFANYLLVVFQKHIAKRFKCCSIFQOEAPERASSYTRSTGEQELSVGL 352	
RESULT 10		
Q71721 PRELIMINARY; PRT; 352 AA.	Q71721 PRELIMINARY; PRT; 352 AA.	
AC 071721	AC 071721	
DT 05-JUL-2004 (TrEMBLref. 27, Created)	DT 05-JUL-2004 (TrEMBLref. 27, Last sequence update)	
DB 301 GEKFANYLLVVFQKHIAKRFKCCSIFQOEAPERASSYTRSTGEQELSVGL 352	DB 301 GEKFANYLLVVFQKHIAKRFKCCSIFQOEAPERASSYTRSTGEQELSVGL 352	
NCBI_TaxID=46359; C-C chemokine receptor 5.	NCBI_TaxID=46359; C-C chemokine receptor 5.	
SEQUENCE FROM N.A.	SEQUENCE FROM N.A.	
Zhang Y., Ryder O. A., Zhang Y.; Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.	Zhang Y., Ryder O. A., Zhang Y.; Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.	
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.	CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.	
DR EMBL; API7700; AAK435.1; -.	DR EMBL; API7700; AAK435.1; -.	
DR GO; GO:0016021; C:integral to membrane; receptor activity; IEA.	DR GO; GO:0016021; C:integral to membrane; receptor activity; IEA.	
DR GO; GO:0004872; F:receptor activity; IEA.	DR GO; GO:0004872; F:receptor activity; IEA.	
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin.. . ; IEA.	DR GO; GO:0007186; P:G-protein coupled receptor protein signalin.. . ; IEA.	
DR InterPro; IPR002240; CC_5 receptor.	DR InterPro; IPR002240; CC_5 receptor.	
DR InterPro; IPR000276; GPCR.	DR InterPro; IPR000276; GPCR.	
DR Pfam; PF00001; 7tm_1; 1.	DR Pfam; PF00001; 7tm_1; 1.	
DR PRINTS; PR00657; CCHEMOKINER.	DR PRINTS; PR00657; CCHEMOKINER.	
DR PRINTS; PR01110; CHEMOKINERS.	DR PRINTS; PR01110; CHEMOKINERS.	
DR PRINTS; PR00237; GPRRHODOPSN.	DR PRINTS; PR00237; GPRRHODOPSN.	
DR PROSITE; PS00237; G PROTEIN RECEPTOR_F1_1;	DR PROSITE; PS00237; G PROTEIN RECEPTOR_F1_1;	
DR PROSITE; PS52626; G PROTEIN RECEPTOR_F1_2;	DR PROSITE; PS52626; G PROTEIN RECEPTOR_F1_2;	
KW G-Protein coupled receptor; Receptor; Transmembrane.	KW G-Protein coupled receptor; Receptor; Transmembrane.	
FT NON_TER 352	FT NON_TER 352	

SQ	SEQUENCE	352 AA;	40466 MW;	3EFFPAC7ABAELD4FB CRC64;				
	Query Match	98.8%;	Score 1818;	DB 2;	Length 352;			
	Best Local Similarity	98.8%;	Pred. No. 5.3e-104;					
	Matches	347;	Conservative	3;	Mismatches	0;		
Qy	1 MDYQVSSPIIDNYNTSEPCOKINTQIAARLLPPLSIVFIFGVGNMLVILILINCKR 60							
Db	61 LKSMTDIYLNLALASDLPFLLTIPFWAHYAAQDFGNTMCQLLTGLYFGFPGSIFII 120							
Qy	1 MDYQVSSPIIDNYNTSEPCOKINTQIAARLLPPLSIVFIFGVGNMLVILILINCKR 60							
Db	61 LKSMTDIYLNLALASDLPFLLTIPFWAHYAAQDFGNTMCQLLTGLYFGFPGSIFII 120							
Qy	121 LLTIDRYLAVVHAVALKARTVTGVVTSVITWWAVFASLPGIIFTRSQEGHLYTCSS 180							
Db	121 LLTIDRYLAVVHAVALKARTVTGVVTSVITWWAVFASLPGIIFTRSQEGHLYTCSS 180							
Qy	181 HFPYSQYQFWNPKTFLKIVLPLVMVCIYSGILKTLRCRNEKEGRHRAVLIFTI 240							
Db	181 HFPYSQYQFWNPKTFLKIVLPLVMVCIYSGILKTLRCRNEKEGRHRAVLIFTI 240							
Qy	241 MIVYFLFWAPYNVILLLNTFOBFGLNCSNSNLDQAMQVTELGMTHCINPVIAYV 300							
Db	241 MIVYFLFWAPYNVILLLNTFOBFGLNCSNSNLDQAMQVTELGMTHCINPVIAYV 300							
Qy	301 GEKFKNYLLVFFQKHIAKRFCCKCSIFQQEAPERASSVYTRSTGEQEVISVGL 352							
Db	301 GEKFKNYLLVFFQKHIAKRFCCKCSIFQQEAPERASSVYTRSTGEQEVISVGL 352							
	RESULT 13							
	Q9X599							
	ID Q9X599; PRELIMINARY;							
	AC Q9X599; PRT; 352 AA.							
	DT 01-NOV-1999 (TREMBrel_12, Created)							
	DT 01-MAR-2004 (TREMBrel_26, Last sequence update)							
	DT 01-MAR-2004 (TREMBrel_26, Last annotation update)							
	DB CCR5 receptor (Fragment).							
	OS Name=CCRS; Pan troglodytes (Chimpanzee); Bukaryota; Metazoa; Chordata; Primates; Catarrhini; Hominidae; Pan. [1]							
	NCBI_TaxID=9538; RN 1							
	RP SEQUENCE FROM N.A. MEDLINE=99210133; PubMed=1019578; DOI=10.1089/088922993111231; RX RA Salasena N.K.; Wang B.; Novembre F.J.; Bolton W.; Smit T.; Lal R.B.; RT "Species-specific changes in the CCR5 gene from African and Asian nonhuman primates."; RL AIDS Res. Hum. Retroviruses 15:479-483 (1999). CC -1 SUBCELLULAR LOCATION: Integral membrane protein (By similarity). DR EMBL; AF10521; AAD20501.1; -; SIMILARITY: Belongs to family 1 of G-protein coupled receptors. DR GO: GO:0016021; C: integral to membrane; IEA. DR GO: GO:0016433; P: C-C chemokine receptor activity; IEA. DR GO: GO:0001544; P: rhodopsin-like receptor activity; IEA. DR GO: GO:007186; P: G-protein coupled receptor protein signalin. . . ; IEA. DR InterPro; IPRO002240; CC 5 receptor. DR InterPro; IPRO00276; GPCR_Rhodpsn. DR PRINTS; PR000557; CCCRHEOKINER. DR PRINTS; PR00110; CHEMOKINERS. DR PRINTS; PR00337; GPCR_Rhodopsn. DR PROSITE; PS00237; G PROTEIN RECEPTOR_F1; 1. DR PROSITE; PS5262; G PROTEIN RECEPTOR_F1; 1. KW G-protein coupled receptor; Receptor; Transmembrane. SQ SEQUENCE 352 AA; 40529 MW; 1BE66868FEAE7ADD CRC64;							
	Query Match	98.7%;	Score 1817;	DB 2;	Length 352;			
	Best Local Similarity	98.3%;	Pred. No. 6.1e-104;					
	Matches	346;	Conservative	3;	Mismatches	3;	Indels	0;
Qy	1 MDYQVSSPIIDNYNTSEPCOKINTQIAARLLPPLSIVFIFGVGNMLVILILINCKR 60							

Db	1 MDYQVSSPPTIDIYTSEPKQKNTVKQIAARLLPLPLSVLFIGFVGMLVILLINKR	60	PT	TRANSMEM	199	218	5 (Potential).		
			PT	DOMAIN	219	235	Cytoplasmic (Potential).		
Qy	61 LKSMPTDIYLINLAISDLFFLTVTYPEWAHYLAQDQDFGTMQCOLTGLYFIGFGSGIFFII	120	FT	TRANSMEM	236	260	6 (Potential).		
			FT	DOMAIN	261	277	Extracellular (Potential).		
Db	61 LKSMPTDIYLINLAISDLFFLTVTYPEWAHYAAQDQDFGTMQCOLTGLYFIGFGSGIFFII	120	FT	TRANSMEM	278	301	7 (Potential).		
			FT	DOMAIN	302	352	Cytoplasmic (Potential).		
Qy	121 LLTIDRYLAVHAYFALKARTVTGGVTSVITWAVASLPLGIPIPSQKEGLHYTCS	180	FT	DISULFID	101	178	By similarity.		
			FT	MOD-RES	3	3	Sulfotyrosine (By similarity).		
Db	121 LLTIDRYLAVHAYFALKARTVTGGVTSVITWAVASLPLGIPIPSQKEGLHYTCS	180	FT	MOD-RES	10	10	Sulfotyrosine (By similarity).		
			FT	MOD-RES	14	14	Sulfotyrosine (By similarity).		
Qy	181 HFPYSQYQFWKNFOTPLKIVLGLVPLMVICSGIKLTLRORNECKHRRAVLRFII	240	FT	CARBOHYD	15	15	Sulfotyrosine (By similarity).		
			FT	SEQUENCE	268	288	N-linked (GlcNAc . .) (Potential).		
Db	181 HFPYSQYQFWKNFOTPLKIVLGLVPLMVICSGIKLTLRORNECKHRRAVLRFII	240	SQ	SEQUENCE	352 AA;	40509 MW;	4366148D3A5936F CRC64;		
			Query	Match	98.6%	Score 1816; DB 1; Length 352;			
Qy	241 MIVYPLFWAPVNIVLILLNTQEFQFGLNCCSSNRLDQAMQVTETLGTHCCINPITYAFV	300	Best Local Similarity	97.7%;	Pred. No. 7e-104;	Gaps 0;			
			Matches	344;	Conservative 6;	Mismatches 2;	Indels 0;		
Db	241 MIVYPLFWAPVNIVLILLNTQEFQFGLNCCSSNRLDQAMQVTETLGTHCCINPITYAFV	300	Qy	1 MDYQVSSPPTIDINYYTSEPCQKININVQTKTAARLLPLPLSIVLFIGFGVSNMLVILLINKR	60	1 MDYQVSSPPTIDYTYTSEPCQKININVQTKTAARLLPLPLSIVLFIGFGVSNMLVILLINKR	60		
			Db	1 LKSMTDIYLINLAISDLFFLTVTPFWAHYAAQDQDFGTMQCOLTGLYFIGFGSGIFFII	120	1 LKSMTDIYLINLAISDLFFLTVTPFWAHYAAQDQDFGTMQCOLTGLYFIGFGSGIFFII	120		
Qy	301 GEKPNAYLVPFOKHIAKRPCKCCSIFQOEAPERASSYTRSTGEQESIVGL	352	Qy	61 LKSMTDIYLINLAISDLFFLTVTPFWAHYAAQDQDFGTMQCOLTGLYFIGFGSGIFFII	120	61 LKSMTDIYLINLAISDLFFLTVTPFWAHYAAQDQDFGTMQCOLTGLYFIGFGSGIFFII	120		
			Db	1 LKSMTDIYLINLAISDLFFLTVTPFWAHYAAQDQDFGTMQCOLTGLYFIGFGSGIFFII	120	1 LKSMTDIYLINLAISDLFFLTVTPFWAHYAAQDQDFGTMQCOLTGLYFIGFGSGIFFII	120		
Qy	301 GEKFRNYLLVFQKHIAKRFCKCCSIFQOEAPERASSYTRSTGEQESIVGL	352	Qy	121 LLTIDRYLAVHAYFALKARTVTGGVTSVITWAVASLPLGIPIPSQKEGLHYTCS	180	121 LLTIDRYLAVHAYFALKARTVTGGVTSVITWAVASLPLGIPIPSQKEGLHYTCS	180		
			Db	121 LLTIDRYLAVHAYFALKARTVTGGVTSVITWAVASLPLGIPIPSQKEGLHYTCS	180	121 LLTIDRYLAVHAYFALKARTVTGGVTSVITWAVASLPLGIPIPSQKEGLHYTCS	180		
Qy	301 GEKFRNYLLVFQKHIAKRFCKCCSIFQOEAPERASSYTRSTGEQESIVGL	352	Qy	181 HFPPYSQYQFWKNFOTPLKIVLGLVPLMVICSGIKLTLRORNECKHRRAVLRFII	240	181 HFPPYSQYQFWKNFOTPLKIVLGLVPLMVICSGIKLTLRORNECKHRRAVLRFII	240		
			Db	181 HFPPYSQYQFWKNFOTPLKIVLGLVPLMVICSGIKLTLRORNECKHRRAVLRFII	240	181 HFPPYSQYQFWKNFOTPLKIVLGLVPLMVICSGIKLTLRORNECKHRRAVLRFII	240		
Qy	301 GEKFRNYLLVFQKHIAKRFCKCCSIFQOEAPERASSYTRSTGEQESIVGL	352	Qy	241 MIYVLFQWAPVNIVLILLNTQEFQFGLNCCSSNRLDQAMQVTETLGTHCCINPITYAFV	300	241 MIYVLFQWAPVNIVLILLNTQEFQFGLNCCSSNRLDQAMQVTETLGTHCCINPITYAFV	300		
			Db	241 MIYVLFQWAPVNIVLILLNTQEFQFGLNCCSSNRLDQAMQVTETLGTHCCINPITYAFV	300	241 MIYVLFQWAPVNIVLILLNTQEFQFGLNCCSSNRLDQAMQVTETLGTHCCINPITYAFV	300		
Qy	301 GEKFRNYLLVFQKHIAKRFCKCCSIFQOEAPERASSYTRSTGEQESIVGL	352	Qy	301 GEKFRNYLLVFQKHIAKRFCKCCSIFQOEAPERASSYTRSTGEQESIVGL	352	301 GEKFRNYLLVFQKHIAKRFCKCCSIFQOEAPERASSYTRSTGEQESIVGL	352		
			Db	301 GEKFRNYLLVFQKHIAKRFCKCCSIFQOEAPERASSYTRSTGEQESIVGL	352	301 GEKFRNYLLVFQKHIAKRFCKCCSIFQOEAPERASSYTRSTGEQESIVGL	352		
<hr/>									
RESULT 14									
CCK5_SEMEN									
ID	CSEMEN	STANDARD;	PRT;	352 AA.					
AC	P61757;								
DT	05-JUL-2004	(Rel. 44, Created)							
DT	05-JUL-2004	(Rel. 44, Last sequence update)							
DT	25-OCT-2004	(Rel. 45, Last annotation update)							
DE	C-C chemokine receptor type 5 (C-C CKR-5) (CCR5) .								
DE	Name=CCKRS; Synonyms=CMXBR5;								
OS	Semnopithecus entellus (Hanuman langur).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;								
OC	Mammalia; Butheria; Primates; Catarrhini; Cercopithecidiae; Colobinae;								
OC	Semnopithecus								
OX	NCBI_TaxID=88029;								
RN	SEQUENCE FROM N.A.								
RX	MEDLINE=9941638; PubMed=10486970;								
RX	Zhang Y.-W., Ryder O.A., Zhang Y.-P.								
RT	"Sequence evolution of the CCR5 chemokine receptor gene in primates.";								
RL	Mol. Biol. Evol. 16:1141-1154 (1999).								
CC	- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-beta and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or differentiation.								
CC	- SUBCELLULAR LOCATION: Integral membrane protein.								
CC	- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.								
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (removed). See http://www.isb-sib.ch/announce/ or send an email to licensee@isb-sib.ch).								
CC	DR: EMBL; AFJ77896; AAC43379_1; -								
DR	PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.								
DR	G-protein coupled receptor; Glycoprotein; Sulfation; Transmembrane.								
KW	DOMAIN; PS50262; G_PROTEIN_RECEP_F1_2; 1.								
FT	TRANSMEM 1								
FT	TRANSMEM 31								
FT	TRANSMEM 59								
FT	TRANSMEM 69								
FT	TRANSMEM 90								
FT	TRANSMEM 102								
FT	TRANSMEM 103								
FT	TRANSMEM 125								
FT	TRANSMEM 142								
FT	TRANSMEM 166								
FT	TRANSMEM 167								
FT	TRANSMEM 198								
FT	TRANSMEM 200								
FT	TRANSMEM 201								
FT	TRANSMEM 202								
FT	TRANSMEM 203								
FT	TRANSMEM 204								
FT	TRANSMEM 205								
FT	TRANSMEM 206								
FT	TRANSMEM 207								
FT	TRANSMEM 208								
FT	TRANSMEM 209								
FT	TRANSMEM 210								
FT	TRANSMEM 211								
FT	TRANSMEM 212								
FT	TRANSMEM 213								
FT	TRANSMEM 214								
FT	TRANSMEM 215								
FT	TRANSMEM 216								
FT	TRANSMEM 217								
FT	TRANSMEM 218								
FT	TRANSMEM 219								
FT	TRANSMEM 220								
FT	TRANSMEM 221								
FT	TRANSMEM 222								
FT	TRANSMEM 223								
FT	TRANSMEM 224								
FT	TRANSMEM 225								
FT	TRANSMEM 226								
FT	TRANSMEM 227								
FT	TRANSMEM 228								
FT	TRANSMEM 229								
FT	TRANSMEM 230								
FT	TRANSMEM 231								
FT	TRANSMEM 232								
FT	TRANSMEM 233								
FT	TRANSMEM 234								
FT	TRANSMEM 235								
FT	TRANSMEM 236								
FT	TRANSMEM 237								
FT	TRANSMEM 238								
FT	TRANSMEM 239								
FT	TRANSMEM 240								
FT	TRANSMEM 241								
FT	TRANSMEM 242								
FT	TRANSMEM 243								
FT	TRANSMEM 244								
FT	TRANSMEM 245								
FT	TRANSMEM 246								
FT	TRANSMEM 247								
FT	TRANSMEM 248								
FT	TRANSMEM 249								
FT	TRANSMEM 250								
FT	TRANSMEM 251								
FT	TRANSMEM 252								
FT	TRANSMEM 253								
FT	TRANSMEM 254								
FT	TRANSMEM 255								
FT	TRANSMEM 256								
FT	TRANSMEM 257								
FT	TRANSMEM 258								
FT	TRANSMEM 259								
FT	TRANSMEM 260								
FT	TRANSMEM 261								
FT	TRANSMEM 262								
FT	TRANSMEM 263								
FT	TRANSMEM 264								
FT	TRANSMEM 265								
FT	TRANSMEM 266								
FT	TRANSMEM 267								
FT	TRANSMEM 268								
FT	TRANSMEM 269								
FT	TRANSMEM 270								
FT	TRANSMEM 271								
FT	TRANSMEM 272								
FT	TRANSMEM 273								
FT	TRANSMEM 274								
FT	TRANSMEM 275								
FT	TRANSMEM 276								
FT	TRANSMEM 277								
FT	TRANSMEM 278								
FT	TRANSMEM 279								
FT	TRANSMEM 280								
FT	TRANSMEM 281								
FT	TRANSMEM 282								
FT	TRANSMEM 283								
FT	TRANSMEM 284								
FT	TRANSMEM 285								
FT	TRANSMEM 286								
FT	TRANSMEM 287								
FT	TRANSMEM 288								
FT	TRANSMEM 289								
FT	TRANSMEM 290								
FT	TRANSMEM 291								
FT	TRANSMEM 292								
FT	TRANSMEM 293								
FT	TRANSMEM 294								
FT	TRANSMEM 295								
FT	TRANSMEM 296								
FT	TRANSMEM 297								
FT	TRANSMEM 298								
FT	TRANSMEM 299								
FT	TRANSMEM 300								
FT	TRANSMEM 301								
FT	TRANSMEM 302								
FT	TRANSMEM 303								
FT	TRANSMEM 304								
FT	TRANSMEM 305								
FT	TRANSMEM 306								
FT	TRANSMEM 307								
FT	TRANSMEM 308								
FT	TRANSMEM 309								
FT	TRANSMEM 310								
FT	TRANSMEM 311					</			

the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC	DR	A075443; AAD19855_1;
CC	DR	InterPro; IPR002240; CC_5_Receptor.
CC	DR	InterPro; IPR000355; Chmkin receptor.
CC	DR	Pfam; PF00001; 7tm_1; 1.
CC	DR	PRINTS; PR00237; GPCR_RHODOPSIN.
CC	DR	PROSITE; PS00237; G PROTEIN RECEP_P1_1;
CC	DR	PROSITE; PS50262; G PROTEIN RECEP_P1_2;
CC	KW	G-protein coupled receptor; Glycoprotein; Sulfation; Transmembrane.
CC	FT	DOMAIN 1 30 Extracellular (Potential).
CC	FT	TRANSMEM 31 58 1 (Potential).
CC	FT	DOMAIN 59 69 Cytoplasmic (Potential).
CC	FT	TRANSMEM 69 89 2 (Potential).
CC	FT	DOMAIN 90 102 Extracellular (Potential).
CC	FT	TRANSMEM 102 124 3 (Potential).
CC	FT	TRANSMEM 103 141 Cytoplasmic (Potential).
CC	FT	DOMAIN 125 141 4 (Potential).
CC	FT	TRANSMEM 142 166 Extracellular (Potential).
CC	FT	DOMAIN 167 198 5 (Potential).
CC	FT	TRANSMEM 199 218 Cytoplasmic (Potential).
CC	FT	DOMAIN 219 235 6 (Potential).
CC	FT	TRANSMEM 235 260 Extracellular (Potential).
CC	FT	TRANSMEM 236 277 7 (Potential).
CC	FT	DOMAIN 261 278 Cytoplasmic (Potential).
CC	FT	TRANSMEM 301 301 352 By similarity.
CC	FT	DISULFID 101 178 Sulfonyroine (By similarity).
CC	FT	MOD_RES 3 3 Sulfonyroine (By similarity).
CC	FT	MOD_RES 10 10 Sulfonyroine (By similarity).
CC	FT	MOD_RES 14 14 Sulfonyroine (By similarity).
CC	FT	MOD_RES 15 15 Sulfonyroine (By similarity).
SQ	SEQUENCE	352 AA; 40509 MW; 4366F14D3A5938P CRC64;

Query Match 98 %; Score 1816; DB 1; Length 352;
 Best Local Similarity 97.7%; Pred. No. 7e-104;
 Matches 344; Conservative 6; Nis matches 2; Indels 0; Gaps 0;

Qy	1 MDYQVSSPIVDINTYTSPECOKINVQIAARLLPLPLSLYPIFGVGNNMVLILINCR 60
Db	1 MDYQVSSPTIDYYTSEPCOKINVQIAARLLPLPLSLYPIFGVGNNMVLILINCR 60
Qy	61 LKSMTDIYLNLAIISPLFFLTIVPPWAHYLAQONDGFNTMCQLTGlyTGFPGIFPTI 120
Db	61 LKSMTDIYLNLAIISPLFFLTIVPPWAHYAAQNDGFNTMCQLTGlyTGFPGIFPTI 120
Qy	121 LLTIDRYLAVHNFALKAKRVTFCVTVSVITWVVAFLSLPLGIFTTSOKEGHYTCSS 180
Db	121 LLTIDRYLAVHNFALKAKRVTFCVTVSVITWVVAFLSLPLGIFTTSOKEGHYTCSS 180
Qy	181 HFPYSQYQFWKQNFQTLKIVIGLVPLVMVICSGILTLRCNEKGRHARVLIFTI 240
Db	181 HFPYSQYQFWKQNFQTLKIVIGLVPLVMVICSGILTLRCNEKGRHARVLIFTI 240
Qy	241 MIVYPLFWAPNIVLLNTQEFFGLNCCSSSNRQAMQVETLGMYTCCINPITYAFV 300
Db	241 MIVYPLFWAPNIVLLNTQEFFGLNCCSSSNRQAMQVETLGMYTCCINPITYAFV 300
Qy	301 GEKFRNYLIVFFQRKIAKRFKCCS1FQQAPERASSYTRSTGEQEISVGL 352
Db	301 GEKFRNYLIVFFQRKIAKRFKCCS1FQQAPERASSYTRSTGEQEISVGL 352

Search completed: October 3, 2005, 07:45:50
 Job time : 100 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6	US-10-700-313-2	Human soft
Copyright (c) 1993 - 2005 Compugen Ltd.		
protein - protein search, using SW model		
on: October 3, 2005, 06:08:13 ; Search time 90 Seconds (without alignments) 1512.663 Million cell updates/sec		
effect score: 1841		
sequence: 1 MDYQVSSPIYDINYTTSEPC.....ERASSVYTRSTGEQEISVGL 352		
scoring table: BLOSUM62		
Gapext 10.0 , Gapext 0.5		
searched: 2105692 seqs, 386760381 residues		

卷之三

post-processing: Minimum Match 0*

Maxwell Malcom Ferguson 45 Summerside, 82

```
database : A_Geneseq_16Dec04;*
```

卷之三

* gene see p. 29903

geneseqp2001s:*

* * * * *

7: -Geneseq2003bs:*

8: geneseqp2004s:*

Dred No is the number of records predicted by Channel to have

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

卷之三

Result	Query				DB	ID	Description
	No.	Score	Match	Length			
1	1841	100.0	371	2	AAW22834		Human CCR Human CC
	2	1836	99.7	352	2	AAW27407	Aat27407 Human CCR
	3	1836	99.7	352	2	AAW27123	Aaw27123 Human che
	4	1836	99.7	352	2	AAW23835	Aaw23835 Human CC
	5	1836	99.7	352	2	AAW88232	Aaw88232 HIV-1 co- Aag80111 Human CCR
	6	1836	99.7	352	4	AAG80111	Aae04321 Human che
	7	1836	99.7	352	4	AAB0321	Aab63354 Human CCR
	8	1836	99.7	352	4	AAB83354	Aab27494 Human HIV
	9	1836	99.7	352	4	AAB82948	Aab52828 Human CC
	10	1836	99.7	352	5	AAM52828	Aab03343 Human che
	11	1836	99.7	352	5	ABB03343	Abr58602 Human can
	12	1836	99.7	352	6	ABR58602	Aac29514 Human C-C
	13	1836	99.7	352	6	AA029514	Abp97728 Amino aci
	14	1836	99.7	352	6	ABP97728	Abp81933 Human C-C
	15	1836	99.7	352	6	ABP81933	Ado03341 Human che
	16	1836	99.7	352	7	ADC03341	Adf44882 Human CC
	17	1836	99.7	352	7	ADF44882	Adk17356 Human CCR
	18	1836	99.7	352	7	ADK17356	Adb65192 Human che
	19	1836	99.7	352	7	ADP65192	Adg42778 Human CC
	20	1836	99.7	352	8	ADG42778	Adh60807 Human CC
	21	1836	99.7	352	8	ADH60807	Adm35887 Human che
	22	1836	99.7	352	8	ADM35887	Ado29227 Human GPC
	23	1836	99.7	352	8	ADO29227	Adp12403 Protein e
	24	1836	99.7	352	8	ADP12403	Ado19578 Human PRO
	25	1836	99.7	352	8	ADO19578	Ado19578 Human PRO

卷之三

RESULT 1	AAW3834			
ID	AAW3834	standard; protein:	371 AA.	
XX				
AC	AAW3834;			
XX				
DT	08-JUN-1998	(first entry)		
XX				
DE	Human CC chemokine receptor 5 (CCRS) A127V variant			
XX				
CW	CC chemokine receptor 5; CCR5; G-protein coupled receptor 5; human immunodeficiency virus; HIV; CCR5; therapeu			
KW				

Key	Location/Qualifiers	Domain	Domain	Domain	Domain	Domain	Domain	Domain
	48 . .74	/label= I /note= "transmembrane domain"						
	123 . .145	/label= III /note= "transmembrane domain"						
	162 . .190	/label= IV /note= "transmembrane domain"						
	213 . .238	/label= V /note= "transmembrane domain"						
	257 . .277	/label= VI /note= "transmembrane domain"						
	296 . .319	/label= VII /note= "transmembrane domain"						

PD	04-DEC-1997.	PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.
XX			
PF	28-MAY-1997;		Combadiere C, Feng Y, Berger EA,
XX			Alkhattyib G,
PR	28-MAY-1996;		Murphy PM;
XX			
PI			Broder CC, Kennedy PE;
PI			

XX Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour;
 KW asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy;
 KW diagnosis; leukocyte trafficking; G protein coupled receptor; ligand;
 KW modulator; antibody; human.

XX

OS Homo sapiens.

Key:

PH Location/Qualifiers

FT Domain 1..32 /label= Extracellular_domain

FT Domain 56..67 /label= Intracellular_domain

FT Domain 89..112 /label= Extracellular_domain

FT Domain 125..145 /label= Intracellular_domain

FT Domain 166..191 /label= Extracellular_domain

FT Domain 213..235 /label= Intracellular_domain

FT Domain 259..280 /label= Extracellular_domain

FT Domain 301..352 /label= Intracellular_domain

FT Domain XX

PN WO9722698-A2.

XX 26-JUN-1997.

XX 20-DEC-1996; 96WO-US020759.

XX 20-DEC-1995; 95US-00575967.

PR 07-JUN-1996; 96US-00661393.

PA (ICOS-) ICOS CORP.

PI Gray PW, Schweickart VL, Report CJ;

XX DR WPI:1997341889/31.
 DR N-PSDB; AAT85161.

XX New nucleic acid encoding chemokine receptors 88-2B and 88C - used to
 PT modulate leukocyte trafficking, e.g. for treatment of inflammation,
 PT tumours, viral infections, auto-immune diseases, etc.

XX Claim 16; Page 47-48; 65pp; English.

XX This polypeptide sequence comprises novel human chemokine receptor 88C, a
 CC G protein coupled receptor that is involved in leukocyte trafficking. Its
 CC amino sequence was deduced from a cDNA clone (AAT85161) isolated from a
 CC macrophage library. It shows 62% identity to CCCR1. Chemokine receptor
 CC 88-2B (see AAW27124) has also been identified. 88C and 88-2B receptors
 CC and their polypeptide fragments can be produced in transformed host
 CC cells. The receptors, peptides comprising one or more of the
 CC extracellular or intracellular domains, and anti-receptor antibodies can
 CC be used to modulate receptor activities, particularly ligand and G
 CC protein binding, and are potentially potentially useful in the treatment
 CC of atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
 CC infection, AIDS, inflammatory conditions, pathological immune response,
 CC abnormal haematopoietic processes etc.

XX Sequence 352 AA;

Query Match 99.7%; Score 1836; DB 2; Length 352;
 Best Local Similarity 99.7%; Pred. No. 3.1e-194;
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYQVSSPIVDINYTSBPCKINKQIAARLLPLPLSVPFGVGNMVLILLINCKR 60
 1 MDYQVSSPIVDINYTSBPCKINKQIAARLLPLPLSVPFGVGNMVLILLINCKR 60

Db 61 LKSMTDIYLNLATSDFLFFLTVPWAHYAAQMDFGNTMCQLTGFIGFFSGIFFII 120

Db 61 LKSMTDIYLNLATSDFLFFLTVPWAHYAAQMDFGNTMCQLTGFIGFFSGIFFII 120

QY 121 LLTIDRYLAVVHALKARTVTGTVTGTGTTGTTVAVPASLPGIPTTSOKEGHHTYCSS 180

Db 121 LLTIDRYLAVVHALKARTVTGTVTGTGTTVAVPASLPGIPTTSOKEGHHTYCSS 180

QY 181 HPPSQYQTWNKFQLKIVLGLVPLLVVICSGILKTLLRCRNEKKHRARVLIFTI 240

Db 181 HPPSQYQTWNKFQLKIVLGLVPLLVVICSGILKTLLRCRNEKKHRARVLIFTI 240

QY 241 MIVYFLFWAPYNITVLLNNTFQEFGLNCCSSSNRLDQANQVTTETLGMTHCCINPDIYAFV 300

Db 241 MIVYFLFWAPYNITVLLNNTFQEFGLNCCSSSNRLDQANQVTTETLGMTHCCINPDIYAFV 300

QY 301 GEKFRNYLVEFQRHIAKRFKCCSFQOEAPERASSYVTRSTQEISVGL 352

Db 301 GEKFRNYLVEFQRHIAKRFKCCSFQOEAPERASSYVTRSTQEISVGL 352

RESULT 4

AAW23835 ID AAW23835 standard; protein; 352 AA.

XX AAW23835;

AC AC

XX DT 08-JUN-1998 (first entry)

XX DE Human CC chemokine receptor 5 (CCR5).

XX CC chemokine receptor 5; CCR5; G-protein coupled receptor;

KW human immunodeficiency virus; HIV; CD4; AIDS; therapy; transgenic animal.

XX OS Homo sapiens.

XX Key Location/Qualifiers

FT Domain 29..55 /label= I
 /note= "transmembrane domain"

FT Domain 104..126 /label= III
 /note= "transmembrane domain"

FT Region 109..120 /note= "extracellular loop-1 (Claim 19)"

FT Domain 143..171 /label= IV
 /note= "transmembrane domain"

FT Region 187..210 /note= "transmembrane domain"

FT Domain 194..219 /label= V
 /note= "transmembrane domain"

FT Domain 238..258 /label= VI
 /note= "transmembrane domain"

FT Region 261..276 /note= "extracellular loop-3 (Claim 19)"

FT Domain 277..300 /label= VII
 /note= "transmembrane domain"

PN WO9745543-A2

XX PD 04-DEC-1997.

XX PP 28-MAY-1997; 97WO-US009586.

XX PR 28-MAY-1996; 96US-0018508P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Conbadiere C, Feng Y, Berger EA, Alkhatib G, Murphy PM;

PI Broder CC, Kennedy PE;

Db	181 HFPYSQYQFWKNFQTLKIVILGLVPLWVYCISGILKTLLRCRNEKKRRAVLIFTI 240	Qy	1 MDYQSSPIYDINYTTSEPCQKINVKQIAARLIPPLYSVIFGFVGNMLVILLLINCKR 60
Qy	241 MIVYFLWAPNIVLLINTQEFFGLINCSSNNRLQAMQTTETLGMTCCINPIYAFV 300	Db	1 MDYQSSPIYDINYTTSEPCQKINVKQIAARLIPPLYSVIFGFVGNMLVILLLINCKR 60
Db	241 MIVYFLWAPNIVLLINTQEFFGLINCSSNNRLQAMQTTETLGMTCCINPIYAFV 300	Qy	61 LKSMTDIYLNLASDLFFLIFTVPWAHYLAQDQFGNTMCQLLTGLYFTGFFGIFTI 120
Qy	301 GEKFPRNYLLVFQKHKAKRFRCKCCS1FQKEAPERASSVTRSTGEQISVGL 352	Db	61 LKSMTDIYLNLASDLFFLIFTVPWAHYAAQDQFGNTMCQLLTGLYFTGFFGIFTI 120
Db	* 301 GEKFPRNYLLVFQKHKAKRFRCKCCS1FQKEAPERASSVTRSTGEQISVGL 352	Qy	121 LLTIDRYLAVVHAYEALKARTVTPCSVVTSVITWVAVFAASLPGJLFTRSOKEGHLHYTCSS 180
		Db	121 LLTIDRYLAVVHAYEALKARTVTPCSVVTSVITWVAVFAASLPGJLFTRSOKEGHLHYTCSS 180
RESULT 6		Qy	181 HFPYSQYQFKNPFQTLKIVILGLVPLWVYCISGILKTLLRCRNEKKRRAVLIFTI 240
AAG80111	ID AAG80111 standard; protein; 352 AA.	Db	181 HFPYSQYQFKNPFQTLKIVILGLVPLWVYCISGILKTLLRCRNEKKRRAVLIFTI 240
XX		Db	181 HFPYSQYQFKNPFQTLKIVILGLVPLWVYCISGILKTLLRCRNEKKRRAVLIFTI 240
AC		Qy	241 MIVYFLWAPNIVLLNTQEFGLINCSSNNRLQAMQTTETLGMTCCINPIYAFV 300
DT	17-JAN-2002 (first entry)	Db	241 MIVYFLWAPNIVLLNTQEFGLINCSSNNRLQAMQTTETLGMTCCINPIYAFV 300
XX		Qy	301 GEKPRNYLLVFQKHKAKRFRCKCCS1FOOBAPERASSVYTRSTGEQISVGL 352
DE	Human CCR5 protein.	Db	301 GEKPRNYLLVFQKHKAKRFRCKCCS1FOOBAPERASSVYTRSTGEQISVGL 352
XX			
Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection; inflammation; autoimmune disease; metastasis; bronchial asthma; lupus; chronic bowel inflammation; rheumatoid arthritis; cytostatic; antiinflammatory; antiasthmatic; immunosuppressive; dermatological; antirheumatic; antiarthritic.			
XX			
OS	Homo sapiens.	RESULT 7	
XX		ID AAE04321 standard; protein; 352 AA.	
PN	WO200172810-A2.	XX	
XX		AC AAE04321;	
PD	04-OCT-2001.	XX	
XX		DT 04-SEP-2001 (first entry)	
PF	02-APR-2001; 2001IW0-EP003708.	XX	
XX		DE Human Chemokine receptor (CCR), CC-CCR-5 related protein #2.	
PR	31-MAR-2000; 2000DB-01016013.	XX	
XX		KW Human; transformed mammalian cell; CD4; reporter gene; translocation; human immuno deficiency virus; HIV; long terminal repeat; LTR; therapy; chemokine receptor; CCR; cellular dysfunction; HIV infection; cofactor; CC-CCR-5; envelope glycoprotein; anti-HIV.	
PA	(IPPP) IPF PHARM GMBH.	XX	
PA (FORS/)	FORSSMANN U.	XX	
XX		OS Homo sapiens.	
PI	Forssmann W, Adermann K, Heitland A, Spodsborg N;	XX	
XX		PN US6258527-B1.	
PT	Diagnostic agent containing two or more receptor-specific ligands, useful for detecting tumors, inflammation etc., also therapeutic use of ligand inhibitors.	XX	
XX		PD 10-JUL-2001.	
DR	WPI; 2001-626256/72.	XX	
XX		PD 21-MAY-1997; 970US-00061105.	
PS Disclosure; Page 10; 26pp; German.		XX	
PS		PR 20-MAY-1996; 96US-0017157P.	
XX		PR 19-JUN-1996; 96US-0020043P.	
CC	This invention describes a novel diagnostic agent (A) comprising at least two different ligands (I) for receptors (II) that are implicated in disease. (A) are used for the diagnosis of tumors (especially colorectal or prostatic), organ rejection, inflammation and autoimmune diseases. Also inhibitors of (I) are used therapeutically against tumors (and their metastases), inflammation (particularly bronchial asthma or chronic bowel inflammation), or autoimmune diseases (rheumatoid arthritis or lupus), where the (cardio)vascular lymphatic, respiratory, nervous, digestive, endocrine, motor or urogenital systems or skin are affected, and bone marrow diseases. The products of the invention are chemokine derivatives which have cytosstatic, antiinflammatory, antiasthmatic, immunosuppressive, dermato logical, antirheumatic, antiarthritic. Chemokines act on specific tumor and inflammatory cells through a constellation of chemokine receptors (CR), which control migration and proliferation of these cells. AAG80128 represents human chemokine fragments used to illustrate the method of the invention	XX	
CC	Sequence 352 AA;	XX	
Query Match	99.7%	Score 1836; DB 4; Length 352;	
Best Local Similarity	99.7%	Pred. No. 3.1e-194; Indels 0; Mismatches 1;	
Matches 351; Conservative		Gaps 0;	

The present invention relates to transformed mammalian cell that contains a gene encoding CD4, a construct encoding a reporter gene under the regulation of an human immunodeficiency virus (HIV) long terminal repeat (LTR) and that has been transduced with a vector encoding a human chemokine receptor (CCR) where the CD4 and the CCR are present on the cell surface of transformed mammalian cell. The invention is useful for identifying drugs or antibodies that interfere with the translocation of

Disclosure; Col 47-50; 37pp; English.

CC The present invention relates to transformed mammalian cell that contains a gene encoding CD4, a construct encoding a reporter gene under the regulation of an human immunodeficiency virus (HIV) long terminal repeat (LTR) and that has been transduced with a vector encoding a human chemokine receptor (CCR) where the CD4 and the CCR are present on the cell surface of transformed mammalian cell. The invention is useful for identifying drugs or antibodies that interfere with the translocation of

CC Disclosure; Col 47-50; 37pp; English.

CC The present invention relates to transformed mammalian cell that contains a gene encoding CD4, a construct encoding a reporter gene under the regulation of an human immunodeficiency virus (HIV) long terminal repeat (LTR) and that has been transduced with a vector encoding a human chemokine receptor (CCR) where the CD4 and the CCR are present on the cell surface of transformed mammalian cell. The invention is useful for identifying drugs or antibodies that interfere with the translocation of

CC HIV into transformed mammalian cell or for identifying a human chemokine
 CC receptor that facilitates the infection of a particular HIV strain into
 CC the transformed mammalian cell. Compounds identified can be used to treat
 CC cellular dysfunction and to prevent or combat HIV infection. The present
 CC sequence is a human chemokine receptor (CCR), CC-CCR-5 related protein.
 CC CCR-5 is the principal cofactor for entry mediated by the envelope
 XX glycoproteins of primary macrophage-tropic strains of HIV-1.

Sequence 352 AA;

Query Match 99.7%; Score 1836; DB 4; Length 352;
 Best Local Similarity 99.7%; Pred. No. 3.1e-194;
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYQSSPIVDINYTSEPCQINKVKIAARLPLPVLVIFEVGMNLVILLINCKR 60
 Db 1 MDYQSSPIVDINYTSEPCQINKVKIAARLPLPVLVIFEVGMNLVILLINCKR 60
 QY 61 LKSMTDIYLNLIAISDLFFLITVPEWAHYLAQMDFGNMCQQLTGLXFIGFGSGIFII 120
 Db 61 LKSMTDIYLNLIAISDLFFLITVPEWAHYLAQMDFGNMCQQLTGLXFIGFGSGIFII 120
 QY 121 LLTIDRYLAVVHAPEALKARTVTFGIVTSVTTWVAVFASLPGIFTQSKEGHYTCSS 180
 Db 121 LLTIDRYLAVVHAPEALKARTVTFGIVTSVTTWVAVFASLPGIFTQSKEGHYTCSS 180
 QY 181 HFPYSOQEMKNFQTLKIVLGNVPLIIVVICSGILKTKLICRNEKPKHRAVLITI 240
 Db 181 HFPYSOQEMKNFQTLKIVLGNVPLIIVVICSGILKTKLICRNEKPKHRAVLITI 240
 QY 241 MIVYFLWAPVNIVLNLQQEFFFQNLNCSSSNLDQAMQVETLGMTHCINPIIYAFV 300
 Db 241 MIVYFLWAPVNIVLNLQQEFFFQNLNCSSSNLDQAMQVETLGMTHCINPIIYAFV 300
 QY 301 GEKFARNYLLVFQKHIARKRFCKCCSIIFQOEAPERASSVYTRSTGEQEISVGL 352
 Db 301 GEKFARNYLLVFQKHIARKRFCKCCSIIFQOEAPERASSVYTRSTGEQEISVGL 352

RESULT 8

AAB83354 standard; protein; 352 AA.

AC AAB83354;

XX DT 09-OCT-2001 (first entry)

XX DE Human CCR5 protein sequence.

XX Chemotactic chemokine receptor 5; gp120; CD4; therapy; HIV; CCR5;
 KW human immunodeficiency virus; anti-inflammatory disease; human.
 XX Homo sapiens.

XX PN EP1118858-A2.

XX PD 25-JUL-2001.

XX PF 03-JAN-2001; 2001EP-00300020.

XX PR 12-JAN-2000; 2000GB-0000059.

PR 12-JAN-2000; 2000GB-0000061.

PR 12-JAN-2000; 2000GB-0000063.

XX (PFIZ) PFIZER LTD.

PA (PFIZ) PFIZER INC.

XX PI Dobbs S, Perros M, Rickett GA;

XX DR WPI: 2001-477088/52.

DR N-PSDB; AAF87099.

XX PT Determining if an agent can modulate CCR5-gp120 interaction, comprises

PT incubating the agent with CCR5 and gp120 and determining if the agent
 PT modulates the interaction.

XX Claim 1; Page 110; 113pp; English.

This sequence represents the human CCR5 protein sequence. The invention
 CC relates to a method for determining whether an agent is capable of
 CC modulating the interaction of chemotactic chemokine receptor 5 (CCR5)
 CC with gp120, comprising incubating the agent with CCR5 and gp120 and
 CC determining whether the agent modulates the interaction, where gp120 is
 CC associated with CD4, and where the interaction is a low affinity binding.
 CC The method is used to identify an agent capable of modulating the
 CC interaction of CCR5 with gp120. An agent identified by the method is used
 CC to prepare a pharmaceutical composition for the treatment of a disease or
 CC condition associated with CCR5 and gp120 interaction, to treat a subject
 CC with a disease or condition associated with CCR5 and gp120 interaction,
 CC and for preparing a pharmaceutical for treating human immunodeficiency
 CC virus (HIV). It can also be treated anti-inflammatory diseases. The method
 CC is commercially useful, amenable to high throughput screening, and
 CC detects interaction of gp120 with cells expressing only CCR5

XX Sequence 352 AA;

Query Match 99.7%; Score 1836; DB 4; Length 352;
 Best Local Similarity 99.7%; Pred. No. 3.1e-194;
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1 MDYQSSPIVDINYTSEPCQINKVKIAARLPLPVLVIFEVGMNLVILLINCKR 60	Db	1 MDYQSSPIVDINYTSEPCQINKVKIAARLPLPVLVIFEVGMNLVILLINCKR 60
QY	61 LKSMTDIYLNLIAISDLFFLITVPEWAHYLAQMDFGNMCQQLTGLXFIGFGSGIFII 120	Db	61 LKSMTDIYLNLIAISDLFFLITVPEWAHYLAQMDFGNMCQQLTGLXFIGFGSGIFII 120
QY	121 LLTIDRYLAVVHAPEALKARTVTFGIVTSVTTWVAVFASLPGIFTQSKEGHYTCSS 180	Db	61 LLTIDRYLAVVHAPEALKARTVTFGIVTSVTTWVAVFASLPGIFTQSKEGHYTCSS 180
QY	181 HFPYSOQEMKNFQTLKIVLGNVPLIIVVICSGILKTKLICRNEKPKHRAVLITI 240	Db	61 HFPYSOQEMKNFQTLKIVLGNVPLIIVVICSGILKTKLICRNEKPKHRAVLITI 240
QY	241 MIVYFLWAPVNIVLNLQQEFFFQNLNCSSSNLDQAMQVETLGMTHCINPIIYAFV 300	Db	241 MIVYFLWAPVNIVLNLQQEFFFQNLNCSSSNLDQAMQVETLGMTHCINPIIYAFV 300
QY	301 GEKFARNYLLVFQKHIARKRFCKCCSIIFQOEAPERASSVYTRSTGEQEISVGL 352	Db	301 GEKFARNYLLVFQKHIARKRFCKCCSIIFQOEAPERASSVYTRSTGEQEISVGL 352
QY	301 GEKFARNYLLVFQKHIARKRFCKCCSIIFQOEAPERASSVYTRSTGEQEISVGL 352	Db	301 GEKFARNYLLVFQKHIARKRFCKCCSIIFQOEAPERASSVYTRSTGEQEISVGL 352

XX RESULT 9

AAB82948 standard; protein; 352 AA.
 ID AAB82948

XX AC AAB82948;

XX DT 21-DEC-2001 (first entry)

XX DE Human HIV-1 co-receptor CCR5.

KW CCR5: chemokine; co-receptor; human immunodeficiency virus type 1; HIV-1.

KW infection; therapy; vaccine; anti-HIV-1.

OS Homo sapiens.

XX FH Key Binding-site
 FT 2. .18
 PT /note= "binds to HIV-1 gp120"
 XX PN WO200164710-A2.

XX

DB	Human C-C chemokine receptor type 5 (333) protein.
PI	PTI
XX	Human; urological disorder; stress urinary incontinence; prostate cancer
KW	benign prostatic hyperplasia; overactive bladder; oversensitive bladder;
KW	overflow urinary incontinence; gene therapy; nephrotropic prostatitis;
KW	kidney disorder; C-C chemokine receptor type 5; CCR5; Receptor.
XX	
PT	New genes that are up-regulated or down-regulated in cancers, useful as
PT	markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
PT	therapeutic targets for screening drugs for treating these diseases.
XX	
PS	Claim 12; Page 745; 76pp; English.
XX	
CC	The present invention describes an isolated nucleic acid molecule, which
CC	comprises the sequence of any of the genes that are up-regulated or down-
CC	regulated in specific cancers (e.g. about 1031 genes up-regulated in
CC	acute lymphocytic leukemia). ACCY2641 to ACCY2660 represent cancer
CC	related gene nucleotide sequences which encode the proteins given in
CC	ABR5851 to ABR58709. Also described: (1) determining the presence or
CC	absence of a pathological cell in a patient; (2) an expression vector
CC	comprising a nucleic acid molecule described above; (3) a host cell
CC	comprising the vector; (4) an isolated polypeptide, which is encoded by
CC	the nucleic acid; (5) an antibody that specifically binds the polypeptide
CC	of (4); (6) specifically targeting a compound to a pathological cell in a
CC	patient by administering to the patient the antibody above; and (7) a
CC	drug screening assay. The nucleic acid is useful as diagnostic markers or
CC	therapeutic targets. In particular, the nucleic acid is useful for
CC	diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
CC	bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
CC	pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
CC	atherosclerosis and endometriosis. The nucleic acid is also useful in
CC	drug screening, particularly for identifying agents for treating these
XX	
SQ	Sequence 352 AA;
Query	99.7%; Score 1836; DB 6; Length 352;
Best Local Similarity	99.7%; Pred. No. 3_1e-194;
Matches	351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db	1 MDYQVSSPYDINYTTSPCOKINVQKAARLPLPLSVLFIGFVNMLVILINCKR 60 1 MDYQVSSPYDINYTTSPCQINVQKAARLPLPLSVLFIGFVNMLVILINCKR 60
Qy	61 LKSMTDIYLNLTAISDLPLFLTYPFWAHYLAQWDFENTMCQILTGLYPIGPGSGIFFII 120 61 LKSMTDIYLNLTAISDLPLFLTYPFWAHYAAQWDFENTMCQILTGLYFIGFGSGIFFII 120
Db	121 LLTIDRYIAVVAHVAFALKARTTFIGVTVITWAVASLPGIIFTRSQREGLYTCS 180 121 LLTIDRYIAVVAHVAFALKARTTFIGVTVITWAVASLPGIIFTRSQREGLYTCS 180
Qy	181 HPPYSOYCFWKQFOTLKVIGLVLPLVMVICYSGLKTLLRCRNFKRAVLFTI 240 181 HPPYSOYCFWKQFOTLKVIGLVLPLVMVICYSGLKTLLRCRNFKRAVLFTI 240
Db	181 HPPYSOYCFWKQFOTLKVIGLVLPLVMVICYSGLKTLLRCRNFKRAVLFTI 240 181 HPPYSOYCFWKQFOTLKVIGLVLPLVMVICYSGLKTLLRCRNFKRAVLFTI 240
Qy	241 MIVYPLFWAPVNVLLNTFOEPFGLNCCSSNRLQAMQVTETLGMTHCCINPIIYAFV 300 241 MIVYPLFWAPVNVLLNTFOEPFGLNCCSSNRLQAMQVTETLGMTHCCINPIIYAFV 300
Db	241 MIVYPLFWAPVNVLLNTFOEPFGLNCCSSNRLQAMQVTETLGMTHCCINPIIYAFV 300 241 MIVYPLFWAPVNVLLNTFOEPFGLNCCSSNRLQAMQVTETLGMTHCCINPIIYAFV 300
Qy	301 GEKFRNTLVLFQFHIAKRFCCKCSIFQEAPEASSYTRSTGEQEISVGL 352 301 GEKFRNTLVLFQFHIAKRFCCKCSIFQEAPEASSYTRSTGEQEISVGL 352
Db	301 GEKFRNTLVLFQFHIAKRFCCKCSIFQEAPEASSYTRSTGEQEISVGL 352 301 GEKFRNTLVLFQFHIAKRFCCKCSIFQEAPEASSYTRSTGEQEISVGL 352
Qy	RESULT 13 AA029514 ID AAO29514 standard; protein; 352 AA.
Qy	AC XX
Db	27-AUG-2003 (first entry)

RESULT 14 ABP97728 ID ABP97728 standard; protein; 352 AA. XX AC XX DT 28-MAY-2003 (first entry) XX DE Amino acid sequence of human chemokine receptor CCR5. XX KW Human: chemokine receptor; CCR5; viral infection; surface protein; KW respiratory virus infection; respiratory syncytial virus infection; RSV infection; bronchiolitis; bronchitis; pneumonia; asthma. XX OS Homo sapiens. XX PN WO2003014153-A2. XX PD 20-FEB-2003. XX PP 12-AUG-2002; 2002WO-CA001248. XX PR 10-AUG-2001; 2001US-031108BP. PA (TOPI-) TOPIGEN PHARM INC. XX PI Renzi P, Zemoumi K; DR WPI: 2003-256541/25. DR N-PSDB; ABZ68881.	Db 241 MIVYPLFWAPYNIVLLINTFQEPFGLNCSNSNRLQAMQVTETLGMTTHCCINPNTIYAFV 300 Qy 301 GEKFRNYLILVFQKHIAKRFCKCCSIFQEAPEASSYTRSTGEQEISVGL 352 Db 301 GEKFRNYLILVFQKHIAKRFCKCCSIFQEAPEASSYTRSTGEQEISVGL 352	Db 241 MIVYPLFWAPYNIVLLINTFQEPFGLNCSNSNRLQAMQVTETLGMTTHCCINPNTIYAFV 300 Qy 301 GEKFRNYLILVFQKHIAKRFCKCCSIFQEAPEASSYTRSTGEQEISVGL 352 Db 301 GEKFRNYLILVFQKHIAKRFCKCCSIFQEAPEASSYTRSTGEQEISVGL 352
RESULT 15 ABP81933 ID ABP81933 standard; protein; 352 AA. XX AC XX DT 04-MAR-2003 (first entry) XX DE Human C-C chemokine receptor 5 protein SEQ ID NO:352. XX KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; G protein-coupled receptor modulator; antibody; immune-related disease; growth-related disease; cell regeneration-related disease; AIDS; cancer; immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy; osteoporosis; cardiomopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma; KW ulcer. XX OS Homo sapiens. XX PN WO200261087-A2. XX PD 08-AUG-2002. XX PF 19-DEC-2001; 2001WO-US050107. XX PR 19-DEC-2000; 2000US-0257144P. XX PA (LIFB-) LIFESPAN BIOSCIENCES INC. XX PI Burmer GC, Roush CL, Brown JP; XX PR 2003-046718/04. DR N-PSDB; ABZ62781. XX PT New isolated antigenic peptides e.g., for G protein-coupled receptors PT useful for diagnosing and designing drugs for treating conditions PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or PT autoimmune diseases. XX PS Disclosure; Fig 1; 523p; English.	Db 241 MIVYPLFWAPYNIVLLINTFQEPFGLNCSNSNRLQAMQVTETLGMTTHCCINPNTIYAFV 300 Qy 301 GEKFRNYLILVFQKHIAKRFCKCCSIFQEAPEASSYTRSTGEQEISVGL 352 Db 301 GEKFRNYLILVFQKHIAKRFCKCCSIFQEAPEASSYTRSTGEQEISVGL 352	Db 241 MIVYPLFWAPYNIVLLINTFQEPFGLNCSNSNRLQAMQVTETLGMTTHCCINPNTIYAFV 300 Qy 301 GEKFRNYLILVFQKHIAKRFCKCCSIFQEAPEASSYTRSTGEQEISVGL 352 Db 301 GEKFRNYLILVFQKHIAKRFCKCCSIFQEAPEASSYTRSTGEQEISVGL 352
Query Match 99.7%; Score 1836; DB 6; Length 352; Best Local Similarity 99.7%; Pre. No. 3_1e-194; Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Qy 1 MDYQVSSPIVDINYTSSEPOQKINVQKAARLLPPLYSIVFVGMLVILINKR 60 1 MDYQVSSPIVDINYTSSEPOQKINVQKAARLLPPLYSIVFVGMLVILINKR 60 Db 61 LKSMTDIVYLNLALSDLFLFLTYPFWAHLAAQMDFGNTMCQLLTGIVIGFFSGIPTII 120 61 LKSMTDIVYLNLALSDLFLFLTYPFWAHLAAQMDFGNTMCQLLTGIVIGFFSGIPTII 120 Qy 121 LLTIDRYLAVHAYFAKLAKRTTIVGYYVSVITWVAVASLPGIPTTSQKEGLHYTCSS 180 121 LLTIDRYLAVHAYFAKLAKRTTIVGYYVSVITWVAVASLPGIPTTSQKEGLHYTCSS 180 Db 181 HPPYSQYQTKWNFOTLKIVIYLGVPLMWICVSGIKTLLCRNEKKRRAVLFTI 240 181 HPPYSQYQTKWNFOTLKIVIYLGVPLMWICVSGIKTLLCRNEKKRRAVLFTI 240 Qy 181 HPPYSQYQTKWNFOTLKIVIYLGVPLMWICVSGIKTLLCRNEKKRRAVLFTI 240 181 HPPYSQYQTKWNFOTLKIVIYLGVPLMWICVSGIKTLLCRNEKKRRAVLFTI 240 Db 241 MIVYPLFWAPYNIVLLINTFQEPFGLNCSNSNRLQAMQVTETLGMTTHCCINPNTIYAFV 300 Qy 241 MIVYPLFWAPYNIVLLINTFQEPFGLNCSNSNRLQAMQVTETLGMTTHCCINPNTIYAFV 300	Qy 1 MDYQVSSPIVDINYTSSEPOQKINVQKAARLLPPLYSIVFVGMLVILINKR 60 1 MDYQVSSPIVDINYTSSEPOQKINVQKAARLLPPLYSIVFVGMLVILINKR 60 Db 61 LKSMTDIVYLNLALSDLFLFLTYPFWAHLAAQMDFGNTMCQLLTGIVIGFFSGIPTII 120 61 LKSMTDIVYLNLALSDLFLFLTYPFWAHLAAQMDFGNTMCQLLTGIVIGFFSGIPTII 120 Qy 121 LLTIDRYLAVHAYFAKLAKRTTIVGYYVSVITWVAVASLPGIPTTSQKEGLHYTCSS 180 121 LLTIDRYLAVHAYFAKLAKRTTIVGYYVSVITWVAVASLPGIPTTSQKEGLHYTCSS 180 Db 181 HPPYSQYQTKWNFOTLKIVIYLGVPLMWICVSGIKTLLCRNEKKRRAVLFTI 240 181 HPPYSQYQTKWNFOTLKIVIYLGVPLMWICVSGIKTLLCRNEKKRRAVLFTI 240 Qy 181 HPPYSQYQTKWNFOTLKIVIYLGVPLMWICVSGIKTLLCRNEKKRRAVLFTI 240 181 HPPYSQYQTKWNFOTLKIVIYLGVPLMWICVSGIKTLLCRNEKKRRAVLFTI 240

hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode GPCR proteins given in ABP81675 to ABP82018, which are used in the exemplification of the present invention

xx

Sequence 352 AA;

Query Match	99.7%	Score 1836;	DB 6;	Length 352;
Best Local Similarity	99.7%	Pred. No.	3.1e-194;	
Matches	351;	Conservative	0;	Mismatches 1; Indels 0; Gaps 0;
Db				
Qy	1 MDYQVSSPIVDINYXTSEPCOKINTYKQIAARLLPPYSLVFIFGVGNMVLVILINKER	60		
Db	1 MDYQVSSPIVDINYXTSEPCOKINTYKQIAARLLPPYSLVFIFGVGNMVLVILINKER	60		
Qy	61 LKSMTDIYLNLNAISDFFELLTVPEPWAYLAQWDFGNTMCQLLTGLYFGPFSCIFII	120		
Db	61 LKSMTDIYLNLNAISDFFELLTVPEPWAYAAQWDFGNTMCQLLTGLYFGPFSCIFII	120		
Qy	121 LLTIDRYLAVVHAPVPAKARTVTFGVVTSVITWWAVAFASLPGIIFTRSOKEGHYTCSS	180		
Db	121 LLTIDRYLAVVHAPVPAKARTVTFGVVTSVITWWAVAFASLPGIIFTRSOKEGHYTCSS	180		
Qy	181 HFPYSSQOFWKNPOTLKIVIGLVLPLVMVICSGILKTLRCNEKGHRAVRLIFTI	240		
Db	181 HFPYSSQFWKNPOTLKIVIGLVLPLVMVICSGILKTLRCNEKGHRAVRLIFTI	240		
Qy	241 MIVYPLFWAPYNIVLINTFOEFFGLNCSSSNRLDQAMQVTELGMTTHCCINPIIYATV	300		
Db	241 MIVYPLFWAPYNIVLINTQEFFGLNCSSSNRLDQAMQVTELGMTTHCCINPIIYATV	300		
Qy	301 GEKPNYLLVVFQKHIAKRPKCCS1FQQDAPERASSVYTRSTGEQEISVGL	352		
Db	301 GEKFRNLLVVFQKHIAKRPKCCS1FQQDAPERASSVYTRSTGEQEISVGL	352		

Search completed: October 3, 2005, 07:44:10
 Job time : 96 secs

THIS PAGE BLANK (USPTO)

Copyright GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 3, 2005, 07:30:50 ; Search time 90 Seconds
(without alignments)

1623.565 Million cell updates/sec

Title: US-10-700-313-2

Perfect score: 1841

Sequence: 1 MDYQVSSPIVDINYTTSEPC.....ERASSVYTRSTGEQIBISVGL 352

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1846076 seqs, 415116000 residues

Total number of hits satisfying chosen parameters: 1846076

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:^{*}

1: /cggn2_6/ptodata/2/pubpaa/us07_PUBCOMB.pep:
2: /cggn2_6/ptodata/2/pubpaa/pct NEW PUB.pep:
3: /cggn2_6/ptodata/2/pubpaa/us06_NEW_PUB.pep:
4: /cggn2_6/ptodata/2/pubpaa/us07_PUBCOMB.pep:
5: /cggn2_6/ptodata/2/pubpaa/pctus NEW PUB.pep:
6: /cggn2_6/ptodata/2/pubpaa/us08_NEW PUB.pep:
7: /cggn2_6/ptodata/2/pubpaa/us09_PUBCOMB.pep:
8: /cggn2_6/ptodata/2/pubpaa/us09A_PUBCOMB.pep:
9: /cggn2_6/ptodata/2/pubpaa/us09A_PUBCOMB.pep:
10: /cggn2_6/ptodata/2/pubpaa/us09B_PUBCOMB.pep:
11: /cggn2_6/ptodata/2/pubpaa/us09C_PUBCOMB.pep:
12: /cggn2_6/ptodata/2/pubpaa/us09_NEW_PUB.pep:
13: /cggn2_6/ptodata/2/pubpaa/us10A_PUBCOMB.pep:
14: /cggn2_6/ptodata/2/pubpaa/us10B_PUBCOMB.pep:
15: /cggn2_6/ptodata/2/pubpaa/us10C_PUBCOMB.pep:
16: /cggn2_6/ptodata/2/pubpaa/us10D_PUBCOMB.pep:
17: /cggn2_6/ptodata/2/pubpaa/us10E_PUBCOMB.pep:
18: /cggn2_6/ptodata/2/pubpaa/us10F_NEW_PUB.pep:
19: /cggn2_6/ptodata/2/pubpaa/us11A_PUBCOMB.pep:
20: /cggn2_6/ptodata/2/pubpaa/us11_NEW_PUB.pep:
21: /cggn2_6/ptodata/2/pubpaa/us60_NEW_PUB.pep:
22: /cggn2_6/ptodata/2/pubpaa/us60_PUBCOMB.pep:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

Sequence 1, Appli
Sequence 6, Appli
Sequence 352, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 67, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 4095, Appli
Sequence 4, Appli
Sequence 5, Appli
Sequence 10, Appli
Sequence 4, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 4368, Appli
Sequence 1133, Appli
Sequence 17, Appli
Sequence 477, Appli
Sequence 52, Appli
Sequence 477, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 22, Appli
Sequence 22, Appli

RESULT 1

US-10-419-845-2

; Sequence 2, Application US/10439845
; Publication No. US20030105348A1
; GENERAL INFORMATION:
; APPLICANT: Combadiere et al.,
; TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/439,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/864,458
; FILING DATE: May 28, 1997
; APPLICATION NUMBER: Provisional 60/018,508
; FILING DATE: May 28, 1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hale, Lisa A.
; REGISTRATION NUMBER: 38,347

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1841	100.0	352 14 US-10-439-845-2	Sequence 2, Appli
2	100.0	352 16 US-10-700-313-2	Sequence 2, Appli	
3	1841	100.0	352 17 US-10-846-185-2	Sequence 2, Appli
4	1836	99.7	352 9 US-09-759-841-2	Sequence 2, Appli
5	1836	99.7	352 9 US-09-813-653-15	Sequence 15, Appli
6	1836	99.7	352 9 US-09-795-202-1	Sequence 1, Appli
7	1836	99.7	352 9 US-09-938-719-5	Sequence 5, Appli
8	1836	99.7	352 9 US-09-939-226-5	Sequence 5, Appli
9	1836	99.7	352 9 US-09-938-703-5	Sequence 5, Appli
10	1836	99.7	352 10 US-09-734-221A-14	Sequence 14, Appli
11	1836	99.7	352 13 US-10-106-623-2	Sequence 2, Appli

REFERENCE/DOCKET NUMBER: 08830/030001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619/678-5070
 TELEFAX: 619/678-5099
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 352 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-10-439-845-2

Query Match 100.0%; Score 1841; DB 14; Length 352;
 Best Local Similarity 100.0%; Pred. No. 4.9e-143;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query	Match	Score	DB	Length
Qy	1 MDYQVSSPIYDINYNTSBCPQKINVQQAARLLAPPLYSILVFIGVGNMVLVILLINCKR	1841	14	352
Db	1 MDYQVSSPIYDINYNTSBCPQKINVQQAARLLAPPLYSILVFIGVGNMVLVILLINCKR	1841	14	352
Qy	61 LKSMTDIYLNLAIISDLFELLTIPFWAHYLAQWDFGNTMCQLLTGLPIGFSGIFII	120	61	120
Do	61 LKSMTDIYLNLAIISDLFELLTIPFWAHYLAQWDFGNTMCQLLTGLPIGFSGIFII	120	61	120
Qy	121 LLTIDRYLAVVHAVALKARTTGFVWVSVITWWVAVFASTPGIIFTRSKQEGHLTYCSS	180	121	180
Db	121 LLTIDRYLAVVHAVALKARTTGFVWVSVITWWVAVFASTPGIIFTRSKQEGHLTYCSS	180	121	180
Qy	181 HFPYSQYQWKNFOTLKIVLGLVPLIWMVICSGIILKTLLRCNEKCRHRAVRLIFTI	240	181	240
Db	181 HFPYSQYQWKNFOTLKIVLGLVPLIWMVICSGIILKTLLRCNEKCRHRAVRLIFTI	240	181	240
Qy	241 MIVYFLWAPNVLNLFQEFGLNCCSSRNLDQAMQVETLGTMTHCCINPIIYAFV	300	241	300
Db	241 MIVYFLWAPNVLNLFQEFGLNCCSSRNLDQAMQVETLGTMTHCCINPIIYAFV	300	241	300
Qy	301 GEKFRNYLIVFQRHIAKRFCFKCCS1FQOEAPERASSYTRSTGEQESVGL	352	301	352
Db	301 GEKFRNYLIVFQRHIAKRFCFKCCS1FQOEAPERASSYTRSTGEQESVGL	352	301	352

RESULT 2
 US-10-700-313-2
 Publication No. US2004025785A1
 GENERAL INFORMATION:
 APPLICANT: Combadiere et al.
 TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 4225 Executive Square, Suite 1400
 CITY: La Jolla
 STATE: CA
 COUNTRY: USA
 ZIP: 92037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US10/700,313
 FILING DATE: 31-Oct-2003
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/864,458
 FILING DATE: 28-MAY-1997
 APPLICATION NUMBER: Provisional 60/018,508
 FILING DATE: May 28, 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Haile, Lisa A.
 REGISTRATION NUMBER: 38,347

RESULT 3
 US-10-700-313-2
 Sequence 2, Application US/10700313
 Publication No. US2004025785A1
 GENERAL INFORMATION:
 APPLICANT: Combadiere et al.,
 TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 4225 Executive Square, Suite 1400
 CITY: La Jolla
 STATE: CA
 COUNTRY: USA
 ZIP: 92037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US10/700,313
 FILING DATE: 31-Oct-2003
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/864,458
 FILING DATE: 28-MAY-1997
 APPLICATION NUMBER: Provisional 60/018,508
 FILING DATE: May 28, 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Haile, Lisa A.
 REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: 08830/030001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619/678-5070
 TELEFAX: 619/678-5099
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 352 amino acids
 TYPE: amino acid
 TOPOLogy: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-10-700-313-2

Query Match 100.0%; Score 1841; DB 16; Length 352;
 Best Local Similarity 100.0%; Pred. No. 4.9e-143;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query	Match	Score	DB	Length
Qy	1 MDYQVSSPIYDINYNTSBCPQKINVQQAARLLAPPLYSILVFIGVGNMVLVILLINCKR	60	1	60
Db	1 MDYQVSSPIYDINYNTSBCPQKINVQQAARLLAPPLYSILVFIGVGNMVLVILLINCKR	60	1	60
Qy	61 LKSMTDIYLNLAIISDLFELLTIPFWAHYLAQWDFGNTMCQLLTGLPIGFSGIFII	120	61	120
Do	61 LKSMTDIYLNLAIISDLFELLTIPFWAHYLAQWDFGNTMCQLLTGLPIGFSGIFII	120	61	120
Qy	121 LLTIDRYLAVVHAVALKARTTGFVWVSVITWWVAVFASTPGIIFTRSKQEGHLTYCSS	180	121	180
Db	121 LLTIDRYLAVVHAVALKARTTGFVWVSVITWWVAVFASTPGIIFTRSKQEGHLTYCSS	180	121	180
Qy	181 HFPYSQYQWKNFOTLKIVLGLVPLIWMVICSGIILKTLLRCNEKCRHRAVRLIFTI	240	181	240
Db	181 HFPYSQYQWKNFOTLKIVLGLVPLIWMVICSGIILKTLLRCNEKCRHRAVRLIFTI	240	181	240
Qy	241 MIVYFLWAPNVLNLFQEFGLNCCSSRNLDQAMQVETLGTMTHCCINPIIYAFV	300	241	300
Db	241 MIVYFLWAPNVLNLFQEFGLNCCSSRNLDQAMQVETLGTMTHCCINPIIYAFV	300	241	300
Qy	301 GEKFRNYLIVFQRHIAKRFCFKCCS1FQOEAPERASSYTRSTGEQESVGL	352	301	352
Db	301 GEKFRNYLIVFQRHIAKRFCFKCCS1FQOEAPERASSYTRSTGEQESVGL	352	301	352

RESULT 3
 US-10-700-313-2
 Sequence 2, Application US/10700313
 Publication No. US2004025785A1
 GENERAL INFORMATION:
 APPLICANT: Combadiere et al.,
 TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 4225 Executive Square, Suite 1400
 CITY: La Jolla
 STATE: CA
 COUNTRY: USA
 ZIP: 92037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US10/700,313
 FILING DATE: 31-Oct-2003
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/864,458
 FILING DATE: 28-MAY-1997
 APPLICATION NUMBER: Provisional 60/018,508
 FILING DATE: May 28, 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Haile, Lisa A.
 REGISTRATION NUMBER: 38,347

RESULT 3
 US-10-700-313-2
 Sequence 2, Application US/10700313
 Publication No. US2004025785A1
 GENERAL INFORMATION:
 APPLICANT: Combadiere et al.,
 TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 4225 Executive Square, Suite 1400
 CITY: La Jolla
 STATE: CA
 COUNTRY: USA
 ZIP: 92037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US10/700,313
 FILING DATE: 31-Oct-2003
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/864,458
 FILING DATE: 28-MAY-1997
 APPLICATION NUMBER: Provisional 60/018,508
 FILING DATE: May 28, 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Haile, Lisa A.
 REGISTRATION NUMBER: 38,347

REGISTRATION NUMBER: 38,347
 TELECOMMUNICATION DOCKET NUMBER: 08830/030001
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 352 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-846-185-2

Query Match	100.0%	Score 1841; DB 1
Best Local Similarity	100.0%	Pred. No. 4.9e-14
Matches	352;	Mismatches 0
Qy	MDYQVSSPPIYDINYTSEPCQKINVKVQIAARLLPLPYS	
Db	MDYQVSSPPIYDINYTSEPCQKINVKVQIAARLLPLPYS	
Qy	LKSMTDTLLNIAISDLFLITVPFWAHYLAQWDFGN	
Db	LKSMTDTLLNIAISDLFLITVPFWAHYLAQWDFGN	
Qy	LITIDRYLAVVHVAFLALKARTTTFGVVTSVITWWVAVF	
Db	LITIDRYLAVVHVAFLALKARTTTFGVVTSVITWWVAVF	
Qy	HPPYSQYQFWINQFOTLKIVIGLVLPILVMVTCYSGIL	
Db	HPPYSQYQFWINQFOTLKIVIGLVLPILVMVTCYSGIL	
Qy	MIVYFLFWAPYIVNLVLLNTFOEFGINNCSSSNRLDOA	
Db	MIVYFLFWAPYIVNLVLLNTFOEFGINNCSSSNRLDOA	
Qy	GEKFERNLYLVFFQKHTAKRFCKCCS1FQQEAPERASSV	
Db	GEKFERNLYLVFFQKHTAKRFCKCCS1FQQEAPERASSV	

RESULT 4
US-09-759-841-2
 ; Sequence 2, Application US/09759841
 ; GENERAL INFORMATION:
 ; APPLICANT: Rickett, Graham A.
 ; APPLICANT: Dobbs, Susan
 ; APPLICANT: Perros, Manousos
 ; TITLE OF INVENTION: Assay Method
 ; FILE REFERENCE: PC10348APME
 ; CURRENT APPLICATION NUMBER: US/09/759,841
 ; CURRENT FILING DATE: 2001-01-12
 ; PRIOR APPLICATION NUMBER: GB 0000661.9
 ; PRIOR FILING DATE: 2000-01-12
 ; PRIOR APPLICATION NUMBER: GB 0000663.5
 ; PRIOR FILING DATE: 2000-01-12
 ; PRIOR APPLICATION NUMBER: GB 0000659.3
 ; PRIOR FILING DATE: 2000-01-12
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 2
 ; LENGTH: 352
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
US-09-759-841-2

Query Match	99.7%	Score 1836; DB 9;
Best Local Similarity	99.7%	Pred. No. 1.3e-142
Matches	351;	Mismatches 0

Db 241 MIVYFLFWAPYNTVLLNTPQEFGNLNCSSNRDQAMQVTETLGMTHCCINPIIYAFV 300
 Qy 301 GEKFRNYLLVFQKHIARFKCKCCSIFQOEAPERASSYTRSTGEQSIVGL 352
 Db 301 GEKFRNYLLVFQKHIARFKCKCCSIFQOEAPERASSYTRSTGEQSIVGL 352

RESULT 6
 US-09-796-202-1
 Sequence 1, Application US/09796202
 Patent No. US2002008813A1
 GENERAL INFORMATION:
 APPLICANT: Dragic, Tatjana
 WILLIAM
 TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
 FILE REFERENCE: 2008/61010/JPN/SHS
 CURRENT APPLICATION NUMBER: US/09/796,202
 CURRENT FILING DATE: 2001-02-28
 NUMBER OF SEQ ID NOS: 17
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 1
 LENGTH: 352
 TYPE: PRTE
 ORGANISM: human
 US-09-796-202-1

Query Match 99.7%; Score 1836; DB 9; Length 352;
 Best Local Similarity 99.7%; Pred. No. 1..3e-14;
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 MDYQSSPYIDINYTTSEPCQKINKVKQIAARLLPPLYSLVIFGFVNMLVILINCKR 60
 Db 1 MDYQSSPYIDINYTTSEPCQKINKVKQIAARLLPPLYSLVIFGFVNMLVILINCKR 60
 Qy 61 LKSMTDIYLNLAISDLFELLTYPFWAHYAAQWDFGNTMCQLTGlyFIGFFSGIFFII 120
 Db 61 LKSMTDIYLNLAISDLFELLTYPFWAHYAAQWDFGNTMCQLTGlyFIGFFSGIFFII 120
 Qy 121 LLTIDRYLAIVVHAYFALKARTVTFGVUTSVITWVAFASLPQIIFTSQEGHLHYTCS 180
 Db 121 LLTIDRYLAIVVHAYFALKARTVTFGVUTSVITWVAFASLPQIIFTSQEGHLHYTCS 180
 Qy 181 HFPYSQYQFWKNEFOTLKIVLGLVPLIIVMVICYSGILKTLLRCNEKRRAVRLIFTI 240
 Db 181 HFPYSQYQFWKNEFOTLKIVLGLVPLIIVMVICYSGILKTLLRCNEKRRAVRLIFTI 240
 Qy 241 MIVYFLFWAPYNTVLLNTPQEFGNLNCSSNRDQAMQVTETLGMTHCCINPIIYAFV 300
 Db 241 MIVYFLFWAPYNTVLLNTPQEFGNLNCSSNRDQAMQVTETLGMTHCCINPIIYAFV 300
 Qy 301 GEKFRNYLLVFQKHIARFKCKCCSIFQOEAPERASSYTRSTGEQSIVGL 352
 Db 301 GEKFRNYLLVFQKHIARFKCKCCSIFQOEAPERASSYTRSTGEQSIVGL 352

RESULT 7

US-09-938-719-5
 Sequence 5, Application US/0938719
 Patent No. US20020106742A1
 GENERAL INFORMATION:
 APPLICANT: SAMSON, MICHEL
 PARMENTIER, MARC
 VASSART, GILBERT
 LIBERT, FREDERICK
 TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
 AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Knobbe, Martens, Olson & Bear
 STREET: 620 Newport Center Drive 16th Floor
 CITY: Newport Beach
 STATE: CA

RESULT 8

US-09-939-226-5
 Sequence 5, Application US/0939226
 Patent No. US20020110805A1
 GENERAL INFORMATION:
 APPLICANT: SAMSON, MICHEL
 PARMENTIER, MARC
 VASSART, GILBERT
 LIBERT, FREDERICK
 TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
 AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Knobbe, Martens, Olson & Bear
 STREET: 620 Newport Center Drive 16th Floor
 CITY: Newport Beach
 STATE: CA

COUNTRY: U.S.A.
 ZIP: 92660
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/938,719
 FILING DATE: 24-Aug-2001
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 09/626,939
 FILING DATE: 27-JULY-2000
 ATTORNEY/AGENT INFORMATION:
 NAME: Altman, Daniel E
 REGISTRATION NUMBER: 34,115
 REFERENCE/DOCKET NUMBER: <Unknown>
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 352 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 US-09-938-719-5

Query Match 99.7%; Score 1836; DB 9; Length 352;
 Best Local Similarity 99.7%; Pred. No. 1..3e-14;
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 MDYQSSPYIDINYTTSEPCQKINKVKQIAARLLPPLYSLVIFGFVNMLVILINCKR 60
 Db 1 MDYQSSPYIDINYTTSEPCQKINKVKQIAARLLPPLYSLVIFGFVNMLVILINCKR 60
 Qy 61 LKSMTDIYLNLAISDLFELLTYPFWAHYAAQWDFGNTMCQLTGlyFIGFFSGIFFII 120
 Db 61 LKSMTDIYLNLAISDLFELLTYPFWAHYAAQWDFGNTMCQLTGlyFIGFFSGIFFII 120
 Qy 121 LLTIDRYLAIVVHAYFALKARTVTFGVUTSVITWVAFASLPQIIFTSQEGHLHYTCS 180
 Db 121 LLTIDRYLAIVVHAYFALKARTVTFGVUTSVITWVAFASLPQIIFTSQEGHLHYTCS 180
 Qy 181 HFPYSQYQFWKNEFOTLKIVLGLVPLIIVMVICYSGILKTLLRCNEKRRAVRLIFTI 240
 Db 181 HFPYSQYQFWKNEFOTLKIVLGLVPLIIVMVICYSGILKTLLRCNEKRRAVRLIFTI 240
 Qy 241 MIVYFLFWAPYNTVLLNTPQEFGNLNCSSNRDQAMQVTETLGMTHCCINPIIYAFV 300
 Db 241 MIVYFLFWAPYNTVLLNTPQEFGNLNCSSNRDQAMQVTETLGMTHCCINPIIYAFV 300
 Qy 301 GEKFRNYLLVFQKHIARFKCKCCSIFQOEAPERASSYTRSTGEQSIVGL 352
 Db 301 GEKFRNYLLVFQKHIARFKCKCCSIFQOEAPERASSYTRSTGEQSIVGL 352

COUNTRY: U.S.A.
 ZIP: 92660
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/939,226
 FILING DATE: 24-Aug-2001
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 09/626,939
 FILING DATE: 2000-07-27
 ATTORNEY/AGENT INFORMATION:
 NAME: Altmann, Daniel E.
 REGISTRATION NUMBER: 34,115
 REFERENCE/DOCKET NUMBER: <Unknown>
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 352 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 3-09-939-226-5

Query Match Best Local Similarity Matches 351; Conservative Matches 351;	Score 1836; DB 9; Pred. No. 1-3e-142; 0, Mismatches 1; Indels 0
---	--

```

  1 MDYQVSSPIDYINNTSEPCQKINYKQIAARLPPLYSLVIFGFVNGLMVLIVI
  1 MDYQVSSPIDYINNTSEPCQKINYKQIAARLPPLYSLVIFGFVNGLMVLIVI
  61 LKSMTDIYLNLASDLPFLITVDFWAHLYLAQDQFGNTMCQQLTGLYPIGF
  61 LKSMTDIYLNLASDLPFLITVDFWAHLYAAQDQFGNTMCQQLTGLYPIGF
  121 LLTIDRYLAVHAFVALKARTVPGAVTSVITWVAVFASLPLGIITFRSQQKE
  121 LLTIDRYLAVHAFVALKARTVPGAVTSVITWVAVFASLPLGIITFRSQQKE
  181 HFPYSQYQWMKFOTLKIVLGLVPLIWNVIVCYSGILKTLRCRNEKRRHRA
  181 HFPYSQYQWMKFOTLKIVLGLVPLIWNVIVCYSGILKTLRCRNEKRRHRA
  241 MIVYFLFWPYNIVLLNTFOETFGLNNSSNLQDAMQTVTLLGMTHCC1
  241 MIVYFLFWPYNIVLLNTFOETFGLNNSSNLQDAMQTVTLLGMTHCC1
  301 GEKFRNYLIVFFQRHIAKRFCCKCSIFQOEAPEASSYTRSTGEQEISVGL
  301 GEKFRNYLIVFFQRHIAKRFCCKCSIFQOEAPEASSVTRSTGEQEISVGL
  
```

RESULT 9
 3-09-938-703-5
 Sequence 5, Application US/09398703
 Patent No. US200211087041
 GENERAL INFORMATION:
 APPLICANT: SAMSON, MICHEL
 PAYMENTIER, MARC
 VASSART, GILBERT
 LIBERT, FREDERICK
 TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECH-
 NUMBER OF SEQUENCES: 17
 AND NUCLEIC ACID MOLECULES ENCODING S-

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Knobbe, Martens, Olson & Bear
 STREET: 620 Newport Center Drive 16th Floor
 CITY: Newport Beach
 STATE: CA

COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25 (BFO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,703
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-938-703-5

Query Match	Score 1836 ; Length 352;	DB 9 ; Length 352;	Pred. No. 1..3e-142;
Best Local Similarity	99.7% ;	99.7% ;	Mismatches 0 ;
Matches 351; Conservative	0 ;	0 ;	Indels 0 ; Gaps 0 ;
/			
1 MDYQVSSPIVDINYTTSEPCOKINTQIAARLLPPLYSLYPIFGFVGNNMVLILINCKR	60	60	
1 MDYQVSSPIVDINYTTSEPCOKINTQIAARLLPPLYSLYPIFGFVGNNMVLILINCKR	60	60	
61 LKSMTDIYLINLAISDLFFLTTVPWAHYAAQWDEGNTMCQLLTGLYTFGGFSGTFFII	120	120	
61 LKSMTDIYLINLAISDLFFLTTVPWAHYAAQWDEGNTMCQLLTGLYTFGGFSGTFFII	120	120	
121 LITIDRYLAVVHAVALKARTTFTFGVTVSTIWWAVASLPGIIFTTSOREKGHLYTCSS	180	180	
121 LITIDRYLAVVHAVALKARTTFTFGVTVSTIWWAVASLPGIIFTTSOREKGHLYTCSS	180	180	
181 HPPYSQYQFWKNFQTLKIVIGLVLPILVMVICSGILKTLRCNEKEHRAYRLIFTI	240	240	
181 HPPYSQYQFWKNFQTLKIVIGLVLPILVMVICSGILKTLRCNEKEHRAYRLIFTI	240	240	
241 MIVYFLFWAPYNIVILLNTFOEFFGLANCCSSNRDQAMQTYETLGMTHCCINPIIYAFV	300	300	
241 MIVYFLFWAPYNIVILLNTFOEFFGLANCCSSNRDQAMQTYETLGMTHCCINPIIYAFV	300	300	
301 GEKFRNYLIVFQKHIAKRPKCCSIIFOQQAPERASSVYTRSTGEQEISVGL	352	352	
301 GEKFRNYLIVFQKHIAKRPKCCSIIFOQQAPERASSVYTRSTGEQEISVGL	352	352	

RESULT 9
-09-338-703-5
Sequence 5, Application US/09938703
Patient No. 20020110870A1
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEAR ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA

RESULT 10
US-09-734-221A-14
Sequence 14, Application US/09734221A
; Publication No. US20030096221A1
; GENERAL INFORMATION:
; APPLICANT: LITTMAN, DAN R.
; DENG, HONGKUI
; EILMEIER, WILFRIED
; LANDAU, NATHANIEL R.
; LIU, RONG
; TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
; MACROPHAGE-TROPHIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
; USES THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; COMPANY: A11 Biotechnology Inc. Compania A11 Biotech
; ADDRESS: 111 University Street, Suite 1000, Seattle, WA 98101

Floor
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/734,221A
 FILING DATE: 11-Dec-2000
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/665,020
 FILING DATE: 19-JUN-1996
 APPLICATION NUMBER: US 08/227,319
 FILING DATE: 13-APR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esg, David A.
 REGISTRATION NUMBER: 1049-1-004 N2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-487-5800
 TELEFAX: 201-343-1684
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 352 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 SEQUENCE DESCRIPTION: SEQ ID NO: 14:
 US-09-734-221A-14

Query Match 99.7% Score 1836; DB 10; Length 352;
 Best Local Similarity 99.7%; Pred. No. 1.3e-14;
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

US-10-106-623-2

Qy 1 MDYQSSPYDINYTTSPCQKINVQIAARLIPPLYSVLFQGVNMLVILLINCKR 60
 Db 1 MDYQSSPYDINYTTSPCQKINVQIAARLIPPLYSVLFQGVNMLVILLINCKR 60

Qy 61 LKSMTDIVLNLAISDLFFLTVPFWAHYLAQONDGFNTMCQLTGLYFIGFGSGIFPTI 120
 Db 61 LKSMTDIVLNLAISDLFFLTVPFWAHYAAQONDGFNTMCQLTGLYFIGFGSGIFPTI 120

Qy 121 LLTDRYLAVHVAFLKARTTIVGTVTSVITWVAVASLPGIFTFSQKEGLHYTCSS 180
 Db 121 LLTDRYLAVHVAFLKARTTIVGTVTSVITWVAVASLPGIFTFSQKEGLHYTCSS 180

Qy 181 HFPPSQYQFWKNFOTLKIVTLGLVLPLMVICYSGILKTLLCRNEKRRAVLIFTI 240
 Db 181 HFPPSQYQFWKNFOTLKIVTLGLVLPLMVICYSGILKTLLCRNEKRRAVLIFTI 240

Qy 241 MIYVFLFWAPYNIVLILNTFOEFFGLNCSSSNRLDAMQVTETLGTHCCINPITYAFV 300
 Db 241 MIYVFLFWAPYNIVLILNTFOEFFGLNCSSSNRLDAMQVTETLGTHCCINPITYAFV 300

Qy 301 GEKFRNYLLVFQKHIAKRFCRKCCSIFQOEAPERASSYTRSTGEQSIVGL 352
 Db 301 GEKFRNYLLVFQKHIAKRFCRKCCSIFQOEAPERASSYTRSTGEQSIVGL 352

RESULT 11
 US-10-106-623-2
 ; Sequence 2, Application US/10106623
 ; Publication No. US20020150888A1
 ; GENERAL INFORMATION:

Qy 301 GEKFRNYLLVFQKHIAKRFCRKCCSIFQOEAPERASSYTRSTGEQSIVGL 352
 Db 301 GEKFRNYLLVFQKHIAKRFCRKCCSIFQOEAPERASSYTRSTGEQSIVGL 352

RESULT 12

US-10-086-814-1
*; Sequence 1, Application US/10086814
 Publication No. US20030092632A1*
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; CURRENT APPLICATION NUMBER: US/10/086, 814
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin version 3.1
; SEQ ID NO: 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-086-814-1
Query Match 99.7%; Score 1836; DB 14; Length 352;
Best Local Similarity 99.7%; Pred. No. 1..3e-142;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 1 MDYQSSPIYDINYTTSEPQKINVKQIAARLPLPLSIVFPGVGNMLVILLINKR 60
Db 1 MDYQSSPIYDINYTTSEPQKINVKQIAARLPLPLSIVFPGVGNMLVILLINKR 60
RESULT 14
Query 1 MDYQSSPIYDINYTTSEPQKINVKQIAARLPLPLSIVFPGVGNMLVILLINKR 60
Db 61 LKSMTDIVLNLAISDLFFLITVFWAHYAAQNDFGNTMCQLLTGLYPIGFSGIFFI 120
Db 61 LKSMTDIVLNLAISDLFFLITVFWAHYAAQNDFGNTMCQLLTGLYPIGFSGIFFI 120
Query 121 LLTIDRYLAVHFAVFKARTVTFGVVTSTVWVAVFASLPGLITFTRSQKEGHYTCS 180
Db 121 LLTIDRYLAVHFAVFKARTVTFGVVTSTVWVAVFASLPGLITFTRSQKEGHYTCS 180
Db 121 LLTIDRYLAVHFAVFKARTVTFGVVTSTVWVAVFASLPGLITFTRSQKEGHYTCS 180
Query 181 HFPYSQYQFMKNPQTLLKIVIGLVPLMVICYSGILKTLLRCNEKRRHARVLIFTI 240
Db 181 HFPYSQYQFMKNPQTLLKIVIGLVPLMVICYSGILKTLLRCNEKRRHARVLIFTI 240
Query 241 MIVYFLFWAPNIVLLNTEQFFGLNCESNSRNLDQAMQVTELGTMTHCCINPIIYAFV 300
Db 241 MIVYFLFWAPNIVLLNTEQFFGLNCESNSRNLDQAMQVTELGTMTHCCINPIIYAFV 300
Query 301 GEKFRNYLLVFFQHIAKRFCCKCSIFQOEAPEASSYTRSTGEQESVGL 352
Db 301 GEKFRNYLLVFFQHIAKRFCCKCSIFQOEAPEASSYTRSTGEQESVGL 352
RESULT 15
Query Match 99.7%; Score 1836; DB 14; Length 352;
Best Local Similarity 99.7%; Pred. No. 1..3e-142;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 1 MDYQSSPIYDINYTTSEPQKINVKQIAARLPLPLSIVFPGVGNMLVILLINKR 60
Db 1 MDYQSSPIYDINYTTSEPQKINVKQIAARLPLPLSIVFPGVGNMLVILLINKR 60
Query 61 LKSMTDIVLNLAISDLFFLITVFWAHYAAQNDFGNTMCQLLTGLYPIGFSGIFFI 120
Db 61 LKSMTDIVLNLAISDLFFLITVFWAHYAAQNDFGNTMCQLLTGLYPIGFSGIFFI 120
Query 121 LLTIDRYLAVHFAVFKARTVTFGVVTSTVWVAVFASLPGLITFTRSQKEGHYTCS 180
Db 121 LLTIDRYLAVHFAVFKARTVTFGVVTSTVWVAVFASLPGLITFTRSQKEGHYTCS 180
Db 121 LLTIDRYLAVHFAVFKARTVTFGVVTSTVWVAVFASLPGLITFTRSQKEGHYTCS 180
Query 181 HFPYSQYQFMKNPQTLLKIVIGLVPLMVICYSGILKTLLRCNEKRRHARVLIFTI 240
Db 181 HFPYSQYQFMKNPQTLLKIVIGLVPLMVICYSGILKTLLRCNEKRRHARVLIFTI 240
Query 241 MIVYFLFWAPNIVLLNTEQFFGLNCESNSRNLDQAMQVTELGTMTHCCINPIIYAFV 300
Db 241 MIVYFLFWAPNIVLLNTEQFFGLNCESNSRNLDQAMQVTELGTMTHCCINPIIYAFV 300
RESULT 16
Query Match 99.7%; Score 1836; DB 14; Length 352;
Best Local Similarity 99.7%; Pred. No. 1..3e-142;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 1 MDYQSSPIYDINYTTSEPQKINVKQIAARLPLPLSIVFPGVGNMLVILLINKR 60
Db 1 MDYQSSPIYDINYTTSEPQKINVKQIAARLPLPLSIVFPGVGNMLVILLINKR 60
Query 61 LKSMTDIVLNLAISDLFFLITVFWAHYAAQNDFGNTMCQLLTGLYPIGFSGIFFI 120
Db 61 LKSMTDIVLNLAISDLFFLITVFWAHYAAQNDFGNTMCQLLTGLYPIGFSGIFFI 120
Query 121 LLTIDRYLAVHFAVFKARTVTFGVVTSTVWVAVFASLPGLITFTRSQKEGHYTCS 180
Db 121 LLTIDRYLAVHFAVFKARTVTFGVVTSTVWVAVFASLPGLITFTRSQKEGHYTCS 180
Db 121 LLTIDRYLAVHFAVFKARTVTFGVVTSTVWVAVFASLPGLITFTRSQKEGHYTCS 180
Query 181 HFPYSQYQFMKNPQTLLKIVIGLVPLMVICYSGILKTLLRCNEKRRHARVLIFTI 240
Db 181 HFPYSQYQFMKNPQTLLKIVIGLVPLMVICYSGILKTLLRCNEKRRHARVLIFTI 240
Query 241 MIVYFLFWAPNIVLLNTEQFFGLNCESNSRNLDQAMQVTELGTMTHCCINPIIYAFV 300
Db 241 MIVYFLFWAPNIVLLNTEQFFGLNCESNSRNLDQAMQVTELGTMTHCCINPIIYAFV 300
RESULT 17
Query Match 99.7%; Score 1836; DB 14; Length 352;
Best Local Similarity 99.7%; Pred. No. 1..3e-142;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 1 MDYQSSPIYDINYTTSEPQKINVKQIAARLPLPLSIVFPGVGNMLVILLINKR 60
Db 1 MDYQSSPIYDINYTTSEPQKINVKQIAARLPLPLSIVFPGVGNMLVILLINKR 60
Query 61 LKSMTDIVLNLAISDLFFLITVFWAHYAAQNDFGNTMCQLLTGLYPIGFSGIFFI 120
Db 61 LKSMTDIVLNLAISDLFFLITVFWAHYAAQNDFGNTMCQLLTGLYPIGFSGIFFI 120
Query 121 LLTIDRYLAVHFAVFKARTVTFGVVTSTVWVAVFASLPGLITFTRSQKEGHYTCS 180
Db 121 LLTIDRYLAVHFAVFKARTVTFGVVTSTVWVAVFASLPGLITFTRSQKEGHYTCS 180
Db 121 LLTIDRYLAVHFAVFKARTVTFGVVTSTVWVAVFASLPGLITFTRSQKEGHYTCS 180
Query 181 HFPYSQYQFMKNPQTLLKIVIGLVPLMVICYSGILKTLLRCNEKRRHARVLIFTI 240
Db 181 HFPYSQYQFMKNPQTLLKIVIGLVPLMVICYSGILKTLLRCNEKRRHARVLIFTI 240
Query 241 MIVYFLFWAPNIVLLNTEQFFGLNCESNSRNLDQAMQVTELGTMTHCCINPIIYAFV 300
Db 241 MIVYFLFWAPNIVLLNTEQFFGLNCESNSRNLDQAMQVTELGTMTHCCINPIIYAFV 300
RESULT 18
Query Match 99.7%; Score 1836; DB 14; Length 352;
Best Local Similarity 99.7%; Pred. No. 1..3e-142;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 1 MDYQSSPIYDINYTTSEPQKINVKQIAARLPLPLSIVFPGVGNMLVILLINKR 60
Db 1 MDYQSSPIYDINYTTSEPQKINVKQIAARLPLPLSIVFPGVGNMLVILLINKR 60
Query 61 LKSMTDIVLNLAISDLFFLITVFWAHYAAQNDFGNTMCQLLTGLYPIGFSGIFFI 120
Db 61 LKSMTDIVLNLAISDLFFLITVFWAHYAAQNDFGNTMCQLLTGLYPIGFSGIFFI 120
Query 121 LLTIDRYLAVHFAVFKARTVTFGVVTSTVWVAVFASLPGLITFTRSQKEGHYTCS 180
Db 121 LLTIDRYLAVHFAVFKARTVTFGVVTSTVWVAVFASLPGLITFTRSQKEGHYTCS 180
Db 121 LLTIDRYLAVHFAVFKARTVTFGVVTSTVWVAVFASLPGLITFTRSQKEGHYTCS 180
Query 181 HFPYSQYQFMKNPQTLLKIVIGLVPLMVICYSGILKTLLRCNEKRRHARVLIFTI 240
Db 181 HFPYSQYQFMKNPQTLLKIVIGLVPLMVICYSGILKTLLRCNEKRRHARVLIFTI 240
Query 241 MIVYFLFWAPNIVLLNTEQFFGLNCESNSRNLDQAMQVTELGTMTHCCINPIIYAFV 300
Db 241 MIVYFLFWAPNIVLLNTEQFFGLNCESNSRNLDQAMQVTELGTMTHCCINPIIYAFV 300
RESULT 19
Query Match 99.7%; Score 1836; DB 14; Length 352;
Best Local Similarity 99.7%; Pred. No. 1..3e-142;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 1 MDYQSSPIYDINYTTSEPQKINVKQIAARLPLPLSIVFPGVGNMLVILLINKR 60
Db 1 MDYQSSPIYDINYTTSEPQKINVKQIAARLPLPLSIVFPGVGNMLVILLINKR 60
Query 61 LKSMTDIVLNLAISDLFFLITVFWAHYAAQNDFGNTMCQLLTGLYPIGFSGIFFI 120
Db 61 LKSMTDIVLNLAISDLFFLITVFWAHYAAQNDFGNTMCQLLTGLYPIGFSGIFFI 120
Query 121 LLTIDRYLAVHFAVFKARTVTFGVVTSTVWVAVFASLPGLITFTRSQKEGHYTCS 180
Db 121 LLTIDRYLAVHFAVFKARTVTFGVVTSTVWVAVFASLPGLITFTRSQKEGHYTCS 180
Db 121 LLTIDRYLAVHFAVFKARTVTFGVVTSTVWVAVFASLPGLITFTRSQKEGHYTCS 180
Query 181 HFPYSQYQFMKNPQTLLKIVIGLVPLMVICYSGILKTLLRCNEKRRHARVLIFTI 240
Db 181 HFPYSQYQFMKNPQTLLKIVIGLVPLMVICYSGILKTLLRCNEKRRHARVLIFTI 240
Query 241 MIVYFLFWAPNIVLLNTEQFFGLNCESNSRNLDQAMQVTELGTMTHCCINPIIYAFV 300
Db 241 MIVYFLFWAPNIVLLNTEQFFGLNCESNSRNLDQAMQVTELGTMTHCCINPIIYAFV 300
RESULT 20
Query Match 99.7%; Score 1836; DB 14; Length 352;
Best Local Similarity 99.7%; Pred. No. 1..3e-142;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 1 MDYQSSPIYDINYTTSEPQKINVKQIAARLPLPLSIVFPGVGNMLVILLINKR 60
Db 1 MDYQSSPIYDINYTTSEPQKINVKQIAARLPLPLSIVFPGVGNMLVILLINKR 60
Query 61 LKSMTDIVLNLAISDLFFLITVFWAHYAAQNDFGNTMCQLLTGLYPIGFSGIFFI 120
Db 61 LKSMTDIVLNLAISDLFFLITVFWAHYAAQNDFGNTMCQLLTGLYPIGFSGIFFI 120
Query 121 LLTIDRYLAVHFAVFKARTVTFGVVTSTVWVAVFASLPGLITFTRSQKEGHYTCS 180
Db 121 LLTIDRYLAVHFAVFKARTVTFGVVTSTVWVAVFASLPGLITFTRSQKEGHYTCS 180
Db 121 LLTIDRYLAVHFAVFKARTVTFGVVTSTVWVAVFASLPGLITFTRSQKEGHYTCS 180
Query 181 HFPYSQYQFMKNPQTLLKIVIGLVPLMVICYSGILKTLLRCNEKRRHARVLIFTI 240
Db 181 HFPYSQYQFMKNPQTLLKIVIGLVPLMVICYSGILKTLLRCNEKRRHARVLIFTI 240
Query 241 MIVYFLFWAPNIVLLNTEQFFGLNCESNSRNLDQAMQVTELGTMTHCCINPIIYAFV 300
Db 241 MIVYFLFWAPNIVLLNTEQFFGLNCESNSRNLDQAMQVTELGTMTHCCINPIIYAFV 300
RESULT 21
Query Match 99.7%; Score 1836; DB 14; Length 352;
Best Local Similarity 99.7%; Pred. No. 1..3e-142;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 301 GEKFRNYLLVFQKHIAKRKFCKCCSIFQQEAPERASSYTRSTGEQEISVGL 352

RESULT 15
 US-10-323-314-1
 ; Sequence 1, Application US/10323314
 ; Publication No. US20030139571A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dragic, Tatjana
 ; APPLICANT: Olson, William
 ; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
 ; FILE REFERENCE: 2048/61010-1/PW/MAP/DJK
 ; CURRENT APPLICATION NUMBER: US/10/323-314
 ; NUMBER OF SEQ ID NOS: 17
 ; CURRENT FILING DATE: 2002-12-19
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 1
 ; LENGTH: 352
 ; TYPE: PRT
 ; ORGANISM: human
 US-10-323-314-1

Query Match 99.7% Score 1836; DB 14; Length 352;
 Best Local Similarity 99.7%; Pred. No. 1, 3e-14;
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 MDYQSSPIYDINNYTSEPCQKINKQIAARLPLIYSLVEFVGMMVILLINCKR 60
 Db 1 MDYQSSPIYDINNYTSEPCQKINKQIAARLPLIYSLVEFVGMMVILLINCKR 60
 Qy 61 LKSMTDIYLNLASDLFFLTVPFWAHYLAQONDGFNTMCQLITGLVFIGFSGIFTI 120
 Db 61 LKSMTDIYLNLASDLFFLTVPFWAHYAAQNDGFNTMCQLITGLVFIGFSGIFTI 120
 Qy 121 LLTIDRYLAVVHAVALKARTVTFGVVTSVITVVAFASLPGIFTTSQKEGHYTCS 180
 Db 121 LLTIDRYLAVVHAVALKARTVTFGVVTSVITVVAFASLPGIFTTSQKEGHYTCS 180
 Qy 181 HFPSQYQFMKNFOTLKIVLGLPLJMMVICYSGIILKTLLACPNEKPRHRAVLTII 240
 Db 181 HFPSQYQFMKNFOTLKIVLGLPLJMMVICYSGIILKTLLACPNEKPRHRAVLTII 240
 Qy 241 MIYVPLFLMAPYNIYLLNTEQFFGLNNCSSSNRLDQAMQVETLGMTHTCCTAPIYAFV 300
 Db 241 MIYVPLFLMAPYNIYLLNTEQFFGLNNCSSSNRLDQAMQVETLGMTHTCCTAPIYAFV 300
 Qy 301 GEKFRNYLLVFQKHIAKRKFCKCCSIFQQEAPERASSYTRSTGEQEISVGL 352
 Db 301 GEKFRNYLLVFQKHIAKRKFCKCCSIFQQEAPERASSYTRSTGEQEISVGL 352

Search completed: October 3, 2005, 07:47:26
 Job time : 91 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 3, 2005, 07:34:24 ; Search time 28 Seconds
(without alignments)

Perfect score: 1841
Sequence: 1 MDYQVSSPIYDINYTTSEPC.....BRASSVYTRSTGEQETISVGL 352

Title: US-10-700-313-2

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgcn2_6/.ptodata/1/iaa/5A_COMB.pep:
2: /cgcn2_6/.ptodata/1/iaa/5B_COMB.pep:
3: /cgcn2_6/.ptodata/1/iaa/6A_COMB.pep:
4: /cgcn2_6/.ptodata/1/iaa/6B_COMB.pep:
5: /cgcn2_6/.ptodata/1/iaa/PCUS_COMB.pep:
6: /cgcn2_6/.ptodata/1/iaa/backfiles1.pep:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution:

SUMMARIES

RESULT 1
US-09-087-232A-13

; Sequence 13, Application US/09087232A
; Patent No. 6153311
; GENERAL INFORMATION:
; APPLICANT: Quillent et al.
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR NUMBER OF SEQUENCES: 23
; TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BEQO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/087-232A
; FILING DATE: 28 MAY 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,057
; FILING DATE: 30 MAY 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KOLE, LISA B.
; REGISTRATION NUMBER: 35,225
; REFERENCE/DOCKET NUMBER: AP 31115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 408-2628
; TELEFAX: (212) 765-2519
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

; US-09-087-232A-13
; Sequence 13, Appl
; Sequence 14, Appl
; Sequence 15, Appl
; Sequence 16, Appl
; Sequence 17, Appl
; Sequence 18, Appl
; Sequence 19, Appl
; Sequence 20, Appl
; Sequence 21, Appl
; Sequence 22, Appl
; Sequence 23, Appl
; Sequence 24, Appl
; Sequence 25, Appl
; Sequence 26, Appl
; Sequence 27, Appl

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution:

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1836	99.7	352	3 US-09-087-232A-13	Sequence 13, Appl
2	1836	99.7	352	3 US-08-861-105-14	Sequence 14, Appl
3	1836	99.7	352	3 US-08-575-967A-2	Sequence 15, Appl
4	1836	99.7	352	4 US-08-833-752-5	Sequence 16, Appl
5	1836	99.7	352	4 US-09-796-202-1	Sequence 17, Appl
6	1836	99.7	352	4 US-09-938-719-5	Sequence 18, Appl
7	1836	99.7	352	4 US-08-931-276-2	Sequence 19, Appl
8	1836	99.7	352	4 US-09-939-226B-5	Sequence 20, Appl
9	1830	99.4	352	3 US-09-045-583-52	Sequence 21, Appl
10	1830	99.4	352	4 US-09-534-185-52	Sequence 22, Appl
11	1830	99.4	352	4 US-09-826-509-417	Sequence 23, Appl
12	1828	99.3	352	4 US-09-502-783A-2	Sequence 24, Appl
13	1828	99.3	352	4 US-09-500-784A-2	Sequence 25, Appl
14	1828	99.3	352	4 US-09-339-912A-2	Sequence 26, Appl
15	1828	99.3	352	4 US-09-195-662A-2	Sequence 27, Appl
16	1821	98.9	352	3 US-08-466-343D-2	Sequence 28, Appl
17	1809	98.3	352	3 US-09-517-605-5	Sequence 29, Appl
18	1802	97.9	352	4 US-08-771-276-20	Sequence 30, Appl
19	1541	83.7	354	3 US-08-724-984A-2	Sequence 31, Appl
20	1360	73.9	360	4 US-09-131-827A-20	Sequence 32, Appl
21	1359	73.8	347	1 US-08-461-244-3	Sequence 33, Appl
22	1359	73.8	360	1 US-08-450-393A-4	Sequence 34, Appl
23	1359	73.8	360	3 US-08-446-669-4	Sequence 35, Appl
24	1359	73.8	360	3 US-09-045-583-50	Sequence 36, Appl
25	1359	73.8	360	4 US-09-534-185-50	Sequence 37, Appl
26	1359	73.8	360	4 US-09-131-827A-2	Sequence 38, Appl
27	1359	73.8	360	4 US-09-625-573-4	Sequence 39, Appl

Sequence 4, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 7, Appli
Sequence 8, Appli
Sequence 9, Appli
Sequence 10, Appli
Sequence 11, Appli
Sequence 12, Appli
Sequence 13, Appli
Sequence 14, Appli
Sequence 15, Appli
Sequence 16, Appli
Sequence 17, Appli
Sequence 18, Appli
Sequence 19, Appli
Sequence 20, Appli
Sequence 21, Appli
Sequence 22, Appli
Sequence 23, Appli
Sequence 24, Appli
Sequence 25, Appli
Sequence 26, Appli
Sequence 27, Appli
Sequence 28, Appli
Sequence 29, Appli
Sequence 30, Appli
Sequence 31, Appli
Sequence 32, Appli
Sequence 33, Appli
Sequence 34, Appli
Sequence 35, Appli
Sequence 36, Appli
Sequence 37, Appli
Sequence 38, Appli
Sequence 39, Appli
Sequence 40, Appli
Sequence 41, Appli
Sequence 42, Appli
Sequence 43, Appli
Sequence 44, Appli
Sequence 45, Appli
Sequence 46, Appli
Sequence 47, Appli
Sequence 48, Appli
Sequence 49, Appli
Sequence 50, Appli
Sequence 51, Appli
Sequence 52, Appli
Sequence 53, Appli
Sequence 54, Appli
Sequence 55, Appli
Sequence 56, Appli
Sequence 57, Appli
Sequence 58, Appli
Sequence 59, Appli
Sequence 60, Appli
Sequence 61, Appli
Sequence 62, Appli
Sequence 63, Appli
Sequence 64, Appli
Sequence 65, Appli
Sequence 66, Appli
Sequence 67, Appli
Sequence 68, Appli
Sequence 69, Appli
Sequence 70, Appli
Sequence 71, Appli
Sequence 72, Appli
Sequence 73, Appli
Sequence 74, Appli
Sequence 75, Appli
Sequence 76, Appli
Sequence 77, Appli
Sequence 78, Appli
Sequence 79, Appli
Sequence 80, Appli
Sequence 81, Appli
Sequence 82, Appli
Sequence 83, Appli
Sequence 84, Appli
Sequence 85, Appli
Sequence 86, Appli
Sequence 87, Appli
Sequence 88, Appli
Sequence 89, Appli
Sequence 90, Appli
Sequence 91, Appli
Sequence 92, Appli
Sequence 93, Appli
Sequence 94, Appli
Sequence 95, Appli
Sequence 96, Appli
Sequence 97, Appli
Sequence 98, Appli
Sequence 99, Appli
Sequence 100, Appli
Sequence 101, Appli
Sequence 102, Appli
Sequence 103, Appli
Sequence 104, Appli
Sequence 105, Appli
Sequence 106, Appli
Sequence 107, Appli
Sequence 108, Appli
Sequence 109, Appli
Sequence 110, Appli
Sequence 111, Appli
Sequence 112, Appli
Sequence 113, Appli
Sequence 114, Appli
Sequence 115, Appli
Sequence 116, Appli
Sequence 117, Appli
Sequence 118, Appli
Sequence 119, Appli
Sequence 120, Appli
Sequence 121, Appli
Sequence 122, Appli
Sequence 123, Appli
Sequence 124, Appli
Sequence 125, Appli
Sequence 126, Appli
Sequence 127, Appli
Sequence 128, Appli
Sequence 129, Appli
Sequence 130, Appli
Sequence 131, Appli
Sequence 132, Appli
Sequence 133, Appli
Sequence 134, Appli
Sequence 135, Appli
Sequence 136, Appli
Sequence 137, Appli
Sequence 138, Appli
Sequence 139, Appli
Sequence 140, Appli
Sequence 141, Appli
Sequence 142, Appli
Sequence 143, Appli
Sequence 144, Appli
Sequence 145, Appli
Sequence 146, Appli
Sequence 147, Appli
Sequence 148, Appli
Sequence 149, Appli
Sequence 150, Appli
Sequence 151, Appli
Sequence 152, Appli
Sequence 153, Appli
Sequence 154, Appli
Sequence 155, Appli
Sequence 156, Appli
Sequence 157, Appli
Sequence 158, Appli
Sequence 159, Appli
Sequence 160, Appli
Sequence 161, Appli
Sequence 162, Appli
Sequence 163, Appli
Sequence 164, Appli
Sequence 165, Appli
Sequence 166, Appli
Sequence 167, Appli
Sequence 168, Appli
Sequence 169, Appli
Sequence 170, Appli
Sequence 171, Appli
Sequence 172, Appli
Sequence 173, Appli
Sequence 174, Appli
Sequence 175, Appli
Sequence 176, Appli
Sequence 177, Appli
Sequence 178, Appli
Sequence 179, Appli
Sequence 180, Appli
Sequence 181, Appli
Sequence 182, Appli
Sequence 183, Appli
Sequence 184, Appli
Sequence 185, Appli
Sequence 186, Appli
Sequence 187, Appli
Sequence 188, Appli
Sequence 189, Appli
Sequence 190, Appli
Sequence 191, Appli
Sequence 192, Appli
Sequence 193, Appli
Sequence 194, Appli
Sequence 195, Appli
Sequence 196, Appli
Sequence 197, Appli
Sequence 198, Appli
Sequence 199, Appli
Sequence 200, Appli
Sequence 201, Appli
Sequence 202, Appli
Sequence 203, Appli
Sequence 204, Appli
Sequence 205, Appli
Sequence 206, Appli
Sequence 207, Appli
Sequence 208, Appli
Sequence 209, Appli
Sequence 210, Appli
Sequence 211, Appli
Sequence 212, Appli
Sequence 213, Appli
Sequence 214, Appli
Sequence 215, Appli
Sequence 216, Appli
Sequence 217, Appli
Sequence 218, Appli
Sequence 219, Appli
Sequence 220, Appli
Sequence 221, Appli
Sequence 222, Appli
Sequence 223, Appli
Sequence 224, Appli
Sequence 225, Appli
Sequence 226, Appli
Sequence 227, Appli
Sequence 228, Appli
Sequence 229, Appli
Sequence 230, Appli
Sequence 231, Appli
Sequence 232, Appli
Sequence 233, Appli
Sequence 234, Appli
Sequence 235, Appli
Sequence 236, Appli
Sequence 237, Appli
Sequence 238, Appli
Sequence 239, Appli
Sequence 240, Appli
Sequence 241, Appli
Sequence 242, Appli
Sequence 243, Appli
Sequence 244, Appli
Sequence 245, Appli
Sequence 246, Appli
Sequence 247, Appli
Sequence 248, Appli
Sequence 249, Appli
Sequence 250, Appli
Sequence 251, Appli
Sequence 252, Appli
Sequence 253, Appli
Sequence 254, Appli
Sequence 255, Appli
Sequence 256, Appli
Sequence 257, Appli
Sequence 258, Appli
Sequence 259, Appli
Sequence 260, Appli
Sequence 261, Appli
Sequence 262, Appli
Sequence 263, Appli
Sequence 264, Appli
Sequence 265, Appli
Sequence 266, Appli
Sequence 267, Appli
Sequence 268, Appli
Sequence 269, Appli
Sequence 270, Appli
Sequence 271, Appli
Sequence 272, Appli
Sequence 273, Appli
Sequence 274, Appli
Sequence 275, Appli
Sequence 276, Appli
Sequence 277, Appli
Sequence 278, Appli
Sequence 279, Appli
Sequence 280, Appli
Sequence 281, Appli
Sequence 282, Appli
Sequence 283, Appli
Sequence 284, Appli
Sequence 285, Appli
Sequence 286, Appli
Sequence 287, Appli
Sequence 288, Appli
Sequence 289, Appli
Sequence 290, Appli
Sequence 291, Appli
Sequence 292, Appli
Sequence 293, Appli
Sequence 294, Appli
Sequence 295, Appli
Sequence 296, Appli
Sequence 297, Appli
Sequence 298, Appli
Sequence 299, Appli
Sequence 300, Appli
Sequence 301, Appli
Sequence 302, Appli
Sequence 303, Appli
Sequence 304, Appli
Sequence 305, Appli
Sequence 306, Appli
Sequence 307, Appli
Sequence 308, Appli
Sequence 309, Appli
Sequence 310, Appli
Sequence 311, Appli
Sequence 312, Appli
Sequence 313, Appli
Sequence 314, Appli
Sequence 315, Appli
Sequence 316, Appli
Sequence 317, Appli
Sequence 318, Appli
Sequence 319, Appli
Sequence 320, Appli
Sequence 321, Appli
Sequence 322, Appli
Sequence 323, Appli
Sequence 324, Appli
Sequence 325, Appli
Sequence 326, Appli
Sequence 327, Appli
Sequence 328, Appli
Sequence 329, Appli
Sequence 330, Appli
Sequence 331, Appli
Sequence 332, Appli
Sequence 333, Appli
Sequence 334, Appli
Sequence 335, Appli
Sequence 336, Appli
Sequence 337, Appli
Sequence 338, Appli
Sequence 339, Appli
Sequence 340, Appli
Sequence 341, Appli
Sequence 342, Appli
Sequence 343, Appli
Sequence 344, Appli
Sequence 345, Appli
Sequence 346, Appli
Sequence 347, Appli
Sequence 348, Appli
Sequence 349, Appli
Sequence 350, Appli
Sequence 351, Appli
Sequence 352, Appli
Sequence 353, Appli
Sequence 354, Appli
Sequence 355, Appli
Sequence 356, Appli
Sequence 357, Appli
Sequence 358, Appli
Sequence 359, Appli
Sequence 360, Appli
Sequence 361, Appli
Sequence 362, Appli
Sequence 363, Appli
Sequence 364, Appli
Sequence 365, Appli
Sequence 366, Appli
Sequence 367, Appli
Sequence 368, Appli
Sequence 369, Appli
Sequence 370, Appli
Sequence 371, Appli
Sequence 372, Appli
Sequence 373, Appli
Sequence 374, Appli
Sequence 375, Appli
Sequence 376, Appli
Sequence 377, Appli
Sequence 378, Appli
Sequence 379, Appli
Sequence 380, Appli
Sequence 381, Appli
Sequence 382, Appli
Sequence 383, Appli
Sequence 384, Appli
Sequence 385, Appli
Sequence 386, Appli
Sequence 387, Appli
Sequence 388, Appli
Sequence 389, Appli
Sequence 390, Appli
Sequence 391, Appli
Sequence 392, Appli
Sequence 393, Appli
Sequence 394, Appli
Sequence 395, Appli
Sequence 396, Appli
Sequence 397, Appli
Sequence 398, Appli
Sequence 399, Appli
Sequence 400, Appli
Sequence 401, Appli
Sequence 402, Appli
Sequence 403, Appli
Sequence 404, Appli
Sequence 405, Appli
Sequence 406, Appli
Sequence 407, Appli
Sequence 408, Appli
Sequence 409, Appli
Sequence 410, Appli
Sequence 411, Appli
Sequence 412, Appli
Sequence 413, Appli
Sequence 414, Appli
Sequence 415, Appli
Sequence 416, Appli
Sequence 417, Appli
Sequence 418, Appli
Sequence 419, Appli
Sequence 420, Appli
Sequence 421, Appli
Sequence 422, Appli
Sequence 423, Appli
Sequence 424, Appli
Sequence 425, Appli
Sequence 426, Appli
Sequence 427, Appli
Sequence 428, Appli
Sequence 429, Appli
Sequence 430, Appli
Sequence 431, Appli
Sequence 432, Appli
Sequence 433, Appli
Sequence 434, Appli
Sequence 435, Appli
Sequence 436, Appli
Sequence 437, Appli
Sequence 438, Appli
Sequence 439, Appli
Sequence 440, Appli
Sequence 441, Appli
Sequence 442, Appli
Sequence 443, Appli
Sequence 444, Appli
Sequence 445, Appli
Sequence 446, Appli
Sequence 447, Appli
Sequence 448, Appli
Sequence 449, Appli
Sequence 450, Appli
Sequence 451, Appli
Sequence 452, Appli
Sequence 453, Appli
Sequence 454, Appli
Sequence 455, Appli
Sequence 456, Appli
Sequence 457, Appli
Sequence 458, Appli
Sequence 459, Appli
Sequence 460, Appli
Sequence 461, Appli
Sequence 462, Appli
Sequence 463, Appli
Sequence 464, Appli
Sequence 465, Appli
Sequence 466, Appli
Sequence 467, Appli
Sequence 468, Appli
Sequence 469, Appli
Sequence 470, Appli
Sequence 471, Appli
Sequence 472, Appli
Sequence 473, Appli
Sequence 474, Appli
Sequence 475, Appli
Sequence 476, Appli
Sequence 477, Appli
Sequence 478, Appli
Sequence 479, Appli
Sequence 480, Appli
Sequence 481, Appli
Sequence 482, Appli
Sequence 483, Appli
Sequence 484, Appli
Sequence 485, Appli
Sequence 486, Appli
Sequence 487, Appli
Sequence 488, Appli
Sequence 489, Appli
Sequence 490, Appli
Sequence 491, Appli
Sequence 492, Appli
Sequence 493, Appli
Sequence 494, Appli
Sequence 495, Appli
Sequence 496, Appli
Sequence 497, Appli
Sequence 498, Appli
Sequence 499, Appli
Sequence 500, Appli
Sequence 501, Appli
Sequence 502, Appli
Sequence 503, Appli
Sequence 504, Appli
Sequence 505, Appli
Sequence 506, Appli
Sequence 507, Appli
Sequence 508, Appli
Sequence 509, Appli
Sequence 510, Appli
Sequence 511, Appli
Sequence 512, Appli
Sequence 513, Appli
Sequence 514, Appli
Sequence 515, Appli
Sequence 516, Appli
Sequence 517, Appli
Sequence 518, Appli
Sequence 519, Appli
Sequence 520, Appli
Sequence 521, Appli
Sequence 522, Appli
Sequence 523, Appli
Sequence 524, Appli
Sequence 525, Appli
Sequence 526, Appli
Sequence 527, Appli
Sequence 528, Appli
Sequence 529, Appli
Sequence 530, Appli
Sequence 531, Appli
Sequence 532, Appli
Sequence 533, Appli
Sequence 534, Appli
Sequence 535, Appli
Sequence 536, Appli
Sequence 537, Appli
Sequence 538, Appli
Sequence 539, Appli
Sequence 540, Appli
Sequence 541, Appli
Sequence 542, Appli
Sequence 543, Appli
Sequence 544, Appli
Sequence 545, Appli
Sequence 546, Appli
Sequence 547, Appli
Sequence 548, Appli
Sequence 549, Appli
Sequence 550, Appli
Sequence 551, Appli
Sequence 552, Appli
Sequence 553, Appli
Sequence 554, Appli
Sequence 555, Appli
Sequence 556, Appli
Sequence 557, Appli
Sequence 558, Appli
Sequence 559, Appli
Sequence 560, Appli
Sequence 561, Appli
Sequence 562, Appli
Sequence 563, Appli
Sequence 564, Appli
Sequence 565, Appli
Sequence 566, Appli
Sequence 567, Appli
Sequence 568, Appli
Sequence 569, Appli
Sequence 570, Appli
Sequence 571, Appli
Sequence 572, Appli
Sequence 573, Appli
Sequence 574, Appli
Sequence 575, Appli
Sequence 576, Appli
Sequence 577, Appli
Sequence 578, Appli
Sequence 579, Appli
Sequence 580, Appli
Sequence 581, Appli
Sequence 582, Appli
Sequence 583, Appli
Sequence 584, Appli
Sequence 585, Appli
Sequence 586, Appli
Sequence 587, Appli
Sequence 588, Appli
Sequence 589, Appli
Sequence 590, Appli
Sequence 591, Appli
Sequence 592, Appli
Sequence 593, Appli
Sequence 594, Appli
Sequence 595, Appli
Sequence 596, Appli
Sequence 597, Appli
Sequence 598, Appli
Sequence 599, Appli
Sequence 600, Appli
Sequence 601, Appli
Sequence 602, Appli
Sequence 603, Appli
Sequence 604, Appli
Sequence 605, Appli
Sequence 606, Appli
Sequence 607, Appli
Sequence 608, Appli
Sequence 609, Appli
Sequence 610, Appli
Sequence 611, Appli
Sequence 612, Appli
Sequence 613, Appli
Sequence 614, Appli
Sequence 615, Appli
Sequence 616, Appli
Sequence 617, Appli
Sequence 618, Appli
Sequence 619, Appli
Sequence 620, Appli
Sequence 621, Appli
Sequence 622, Appli
Sequence 623, Appli
Sequence 624, Appli
Sequence 625, Appli
Sequence 626, Appli
Sequence 627, Appli
Sequence 628, Appli
Sequence 629, Appli
Sequence 630, Appli
Sequence 631, Appli
Sequence 632, Appli
Sequence 633, Appli
Sequence 634, Appli
Sequence 635, Appli
Sequence 636, Appli
Sequence 637, Appli
Sequence 638, Appli
Sequence 639, Appli
Sequence 640, Appli
Sequence 641, Appli
Sequence 642, Appli
Sequence 643, Appli
Sequence 644, Appli
Sequence 645, Appli
Sequence 646, Appli
Sequence 647, Appli
Sequence 648, Appli
Sequence 649, Appli
Sequence 650, Appli
Sequence 651, Appli
Sequence 652, Appli
Sequence 653, Appli
Sequence 654, Appli
Sequence 655, Appli
Sequence 656, Appli
Sequence 657, Appli
Sequence 658, Appli
Sequence 659, Appli
Sequence 660, Appli
Sequence 661, Appli
Sequence 662, Appli
Sequence 663, Appli
Sequence 664, Appli
Sequence 665, Appli
Sequence 666, Appli
Sequence 667, Appli
Sequence 668, Appli
Sequence 669, Appli
Sequence 670, Appli
Sequence 671, Appli
Sequence 672, Appli
Sequence 673, Appli
Sequence 674, Appli
Sequence 675, Appli
Sequence 676, Appli
Sequence 677, Appli
Sequence 678, Appli
Sequence 679, Appli
Sequence 680, Appli
Sequence 681, Appli
Sequence 682, Appli
Sequence 683, Appli
Sequence 684, Appli
Sequence 685, Appli
Sequence 686, Appli
Sequence 687, Appli
Sequence 688, Appli
Sequence 689, Appli
Sequence 690, Appli
Sequence 691, Appli
Sequence 692, Appli
Sequence 693, Appli
Sequence 694, Appli
Sequence 695, Appli
Sequence 696, Appli
Sequence 697, Appli
Sequence 698, Appli
Sequence 699, Appli
Sequence 700, Appli
Sequence 701, Appli
Sequence 702, Appli
Sequence 703, Appli
Sequence 704, Appli
Sequence 705, Appli
Sequence 706, Appli
Sequence 707, Appli
Sequence 708, Appli
Sequence 709, Appli
Sequence 710, Appli
Sequence 711, Appli
Sequence 712, Appli
Sequence 713, Appli
Sequence 714, Appli
Sequence 715, Appli
Sequence 716, Appli
Sequence 717, Appli
Sequence 718, Appli
Sequence 719, Appli
Sequence 720, Appli
Sequence 721, Appli
Sequence 722, Appli
Sequence 723, Appli
Sequence 724, Appli
Sequence 725, Appli
Sequence 726, Appli
Sequence 727, Appli
Sequence 728, Appli
Sequence 729, Appli
Sequence 730, Appli
Sequence 731, Appli
Sequence 732, Appli
Sequence 733, Appli
Sequence 734, Appli
Sequence 735, Appli
Sequence 736, Appli
Sequence 737, Appli
Sequence 738, Appli
Sequence 739, Appli
Sequence 740, Appli
Sequence 741, Appli
Sequence 742, Appli
Sequence 743, Appli
Sequence 744, Appli
Sequence 745, Appli
Sequence 746, Appli
Sequence 747, Appli
Sequence 748, Appli
Sequence 749, Appli
Sequence 750, Appli
Sequence 751, Appli
Sequence 752, Appli
Sequence 753, Appli
Sequence 754, Appli
Sequence 755, Appli
Sequence 756, Appli
Sequence 757, Appli
Sequence 758, Appli
Sequence 759, Appli
Sequence 760, Appli
Sequence 761, Appli
Sequence 762, Appli
Sequence 763, Appli

Oy 61 LKSMTDIYLNLATSDLFFLLTYPFWAIIYLAQWDFGNTMCOLLTGLYFIGFGSGITFFI 120 ; MOLECULE TYPE: protein
 Oy 61 LKSMTDIYLNLATSDLFFLLTYPFWAIIYLAQWDFGNTMCOLLTGLYFIGFGSGITFFI 120 ; HYPOTHETICAL: NO
 Db 121 LLTIDRYLAVVHAYFALKARTTIVFGVVTSVITVVAVASLPGIIFTRSQEGLYHTCSS 180 ; ORIGINAL SOURCE:
 Db 121 LLTIDRYLAVVHAYFALKARTTIVFGVVTSVITVVAVASLPGIIFTRSQEGLYHTCSS 180 ; US-08-861-105-14
 Query Match 99.7%; Score 1836; DB 3; Length 352;
 Best Local Similarity 99.7%; Pred. No. 1..1e-14;
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 MDYQVSSPIYDINYTTSEPCOKINVQTAARLLPLYSVLVIFGFVNMLVILILINCKR 60
 Db 1 MDYQVSSPIYDINYTTSEPCOKINVQTAARLLPLYSVLVIFGFVNMLVILILINCKR 60
 Qy 241 MIVYFLFWAPYNTVLLNLTFOEQPFLGCNSSRNLDQAMQVETLGHTHCCINPIITYAFV 300
 Db 241 MIVYFLFWAPYNTVLLNLTFOEQPFLGCNSSRNLDQAMQVETLGHTHCCINPIITYAFV 300
 Qy 301 GEKFPRNYLIVFQKHIAKRCPCKCCSIFQEAPEARRYSTRSGEQLSVGL 352
 Db 301 GEKFPRNYLIVFQKHIAKRCPCKCCSIFQEAPEARRYSTRSGEQLSVGL 352
 RESULT 3
 US-08-861-105-14
 ; Sequence 14, Application US/08861105
 ; GENERAL INFORMATION:
 ; APPLICANT: LITTMAN, DAN R.
 ; APPLICANT: DEENG, HONGRUI
 ; APPLICANT: ELLMEIER, WILFRIED
 ; APPLICANT: LANDAU, NATHANIEL R.
 ; APPLICANT: LIU, RONG
 ; TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
 ; TITLE OF INVENTION: MACROPHAGE-TROPHIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: David A. Jackson, Esq.
 ; STREET: 411 Hackensack Ave, Continental Plaza, 4th
 ; STREET: Floor
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/861,105
 PRIORITY APPLICATION DATA:
 FILING DATE:
 CLASSIFICATION: 436
 PRIOR APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 1049-1-004 N1
 TELEPHONE: 201-487-5800
 TELEFAX: 201-343-1684
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 352 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:

; NAME/KEY: misc_feature
; OTHER INFORMATION: / = "88C amino acid sequence"
US-08-313-2

Query Match 99.7%; Score 1836; DB 3; Length 352;
Best Local Similarity 99.7%; Pred. No. 1..1e-146;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDYQSSPYIDINNYTSEPCOKINKQFAARLLPLYSVPIPGFVGMLVILLINCKR 60
Db 1 MDYQSSPYIDINNYTSEPCOKINKQFAARLLPLYSVPIPGFVGMLVILLINCKR 60

Qy 61 LKSMTDIVLNLAISDLFPLLTVPFWAHYAAQWDFGNTMCQLLGLYFIGFGIFFI 120
Db 61 LKSMTDIVLNLAISDLFPLLTVPFWAHYAAQWDFGNTMCQLLGLYFIGFGIFFI 120

Qy 121 LLTDRYLAVHVFALKARTVFGVVTSGVTSVITVAVASLPGIIFTRSQKEGHYTCS 180
Db 121 LLTDRYLAVHVFALKARTVFGVVTSGVTSVITVAVASLPGIIFTRSQKEGHYTCS 180

Qy 121 LLTDRYLAVHVFALKARTVFGVVTSGVTSVITVAVASLPGIIFTRSQKEGHYTCS 180
Db 121 LLTDRYLAVHVFALKARTVFGVVTSGVTSVITVAVASLPGIIFTRSQKEGHYTCS 180

Qy 181 HFPYSQYQFWKNFQTLKIVIGLVPLLYMVICSGILKTLLRCRNECKHRAVLIFTI 240
Db 181 HFPYSQYQFWKNFQTLKIVIGLVPLLYMVICSGILKTLLRCRNECKHRAVLIFTI 240

Qy 181 HFPYSQYQFWKNFQTLKIVIGLVPLLYMVICSGILKTLLRCRNECKHRAVLIFTI 240
Db 181 HFPYSQYQFWKNFQTLKIVIGLVPLLYMVICSGILKTLLRCRNECKHRAVLIFTI 240

Qy 241 MIVYFLFWAPYNVILLNTPQEFGLNCSSSNRLDAMQVTETLGMTTHCCINPITYAFV 300
Db 241 MIVYFLFWAPYNVILLNTPQEFGLNCSSSNRLDAMQVTETLGMTTHCCINPITYAFV 300

Qy 301 GEKFRNLLVFFQHIAKRFCKCCSIFQOEAPERASSYTRSTGEQSIVGL 352
Db 301 GEKFRNLLVFFQHIAKRFCKCCSIFQOEAPERASSYTRSTGEQSIVGL 352

Qy 301 GEKFRNLLVFFQHIAKRFCKCCSIFQOEAPERASSYTRSTGEQSIVGL 352
Db 301 GEKFRNLLVFFQHIAKRFCKCCSIFQOEAPERASSYTRSTGEQSIVGL 352

RESULT 5
US-09-796-202-1
; Sequence 1, Application US/09796202
; Patent No. 6548336
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SUPATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/PW/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: human
US-09-796-202-1

Query Match 99.7%; Score 1836; DB 4; Length 352;
Best Local Similarity 99.7%; Pred. No. 1..1e-146;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDYQSSPYIDINNYTSEPCOKINKQFAARLLPLYSVPIPGFVGMLVILLINCKR 60
Db 1 MDYQSSPYIDINNYTSEPCOKINKQFAARLLPLYSVPIPGFVGMLVILLINCKR 60

Qy 61 LKSMTDIVLNLAISDLFPLLTVPFWAHYAAQWDFGNTMCQLLGLYFIGFGIFFI 120
Db 61 LKSMTDIVLNLAISDLFPLLTVPFWAHYAAQWDFGNTMCQLLGLYFIGFGIFFI 120

Qy 121 LLTDRYLAVHVFALKARTVFGVVTSGVTSVITVAVASLPGIIFTRSQKEGHYTCS 180
Db 121 LLTDRYLAVHVFALKARTVFGVVTSGVTSVITVAVASLPGIIFTRSQKEGHYTCS 180

Qy 181 HFPYSQYQFWKNFQTLKIVIGLVPLLYMVICSGILKTLLRCRNECKHRAVLIFTI 240
Db 181 HFPYSQYQFWKNFQTLKIVIGLVPLLYMVICSGILKTLLRCRNECKHRAVLIFTI 240

Qy 241 MIVYFLFWAPYNVILLNTPQEFGLNCSSSNRLDAMQVTETLGMTTHCCINPITYAFV 300
Db 241 MIVYFLFWAPYNVILLNTPQEFGLNCSSSNRLDAMQVTETLGMTTHCCINPITYAFV 300

Qy 301 GEKFRNLLVFFQHIAKRFCKCCSIFQOEAPERASSYTRSTGEQSIVGL 352

Db 301 GEKFRNYLLVFFQKTHIAKRFCCKCSIFQQEAPERASSYTRSTGEQESVGL 352 RESULT 6 US-09-938-719-5 ; Sequence 5, Application US/099380719 ; Patent No. 6692938 ; GENERAL INFORMATION : APPLICANT: SAMSON, MICHEL PARMENTIER, MARC VASSART, GILBERT LIBERT, FREDERICK TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR NUMBER OF SEQUENCES: 17 CORRESPONDENCE ADDRESS: Knobbe, Martens, Olson & Bear STREET: 620 Newport Center Drive 16th Floor CITY: Newport Beach STATE: CA COUNTRY: U.S.A. ZIP: 92660 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/938,719 FILING DATE: 24-Aug-2001 PRIORITY APPLICATION DATA: APPLICATION NUMBER: 09/626,939 FILING DATE: 27-JULY-2000 ATTORNEY/AGENT INFORMATION: NAME: Alteman, Daniel E. REGISTRATION NUMBER: 34-115 INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 352 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: Protein SEQUENCE DESCRIPTION: SEQ ID NO: 5: ;US-09-938-719-5

Query Match 99.7%; Score 1836; DB 4; Length 352; Best Local Similarity 99.7%; Pred. No. 1..1e-14; Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Qy 1 MDYQVSSPPIYDINYTSEPCOKINVQKAARLPLPLYSVAFIGFGNMVLVILLINKR 60 Db 1 MDYQVSSPPIYDINYTSEPCQKINVQKAARLPLPLYSVAFIGFGNMVLVILLINKR 60 Qy 61 LKSMTDIYLNLASDLFLFLTYPEWAHYLAQWDFNTMCQLTGFLYFIGPSGIPII 120 Db 61 LKSMTDIYLNLASDLFLFLTYPEWAHYAAQWDFNTMCQLTGFLYFIGPSGIPII 120 Qy 121 LLTDIDRYLAVVHAFALKARTTGFVVVSVITVVAVASLPGIIFTSQKEGLHYTSS 180 Db 121 LLTDIDRYLAVVHAFALKARTTGFVVVSVITVVAVASLPGIIFTSQKEGLHYTSS 180 Qy 181 HFPYSQYQPKWNFQTLKIVLGVLPLLVIVCYSGIILTLCRNBEKGRHRARVLFTI 240 Db 181 HFPYSQYQPKWNFQTLKIVLGVLPLLVIVCYSGIILTLCRNBEKGRHRARVLFTI 240 Qy 241 MIYVFLFWAPYNVILNLTFOEFGFLNCCSSSNRLDOAMQVTETLMTHCCINPITYAFV 300 Db 241 MIYVFLFWAPYNVILNLTFOEFGFLNCCSSSNRLDQMVTETLMTHCCINPITYAFV 300 Qy 301 GEKFRNYLLVFFQKTHIAKRFCCKCSIFQQEAPERASSYTRSTGEQESVGL 352 RESULT 7 US-08-771-276-2 ; Sequence 2, Application US/08771276 ; Patent No. 6797811 ; GENERAL INFORMATION : APPLICANT: Gray, Patrick W. SCHWEICKART, Vicki L. APPLICANT: Report, Carol J. TITLE OF INVENTION: Chemokine Receptor Materials and Methods NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Buron STREET: 6300 Sears Tower, 233 S. Wacker Drive CITY: Chicago STATE: Illinois COUNTRY: USA ZIP: 60606 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/771,276 FILING DATE: ATTORNEY/AGENT INFORMATION: NAME: No. 6797811 and, Greta E. REGISTRATION NUMBER: 35,302 REFERENCE DOCKET NUMBER: 27866/33670 TELECOMMUNICATION INFORMATION: TELEPHONE: 312-474-6300 TELEFAX: 312-474-0448 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 352 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein FEATURE: NAME/KEY: misc feature OTHER INFORMATION: /= "88C amino acid sequence" ;US-08-771-276-2

Query Match 99.7%; Score 1836; DB 4; Length 352; Best Local Similarity 99.7%; Pred. No. 1..1e-14; Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Qy 1 MDYQVSSPPIYDINYTSEPCOKINVQKAARLPLPLYSVAFIGFGNMVLVILLINKR 60 Db 1 MDYQVSSPPIYDINYTSEPCQKINVQKAARLPLPLYSVAFIGFGNMVLVILLINKR 60 Qy 61 LKSMTDIYLNLASDLFLFLTYPEWAHYLAQWDFNTMCQLTGFLYFIGPSGIPII 120 Db 61 LKSMTDIYLNLASDLFLFLTYPEWAHYAAQWDFNTMCQLTGFLYFIGPSGIPII 120 Qy 121 LLTDIDRYLAVVHAFALKARTTGFVVVSVITVVAVASLPGIIFTSQKEGLHYTSS 180 Db 121 LLTDIDRYLAVVHAFALKARTTGFVVVSVITVVAVASLPGIIFTSQKEGLHYTSS 180 Qy 181 HFPYSQYQPKWNFQTLKIVLGVLPLLVIVCYSGIILTLCRNBEKGRHRARVLFTI 240 Db 181 HFPYSQYQPKWNFQTLKIVLGVLPLLVIVCYSGIILTLCRNBEKGRHRARVLFTI 240 Qy 241 MIYVFLFWAPYNVILNLTFOEFGFLNCCSSSNRLDOAMQVTETLMTHCCINPITYAFV 300 Db 241 MIYVFLFWAPYNVILNLTFOEFGFLNCCSSSNRLDQMVTETLMTHCCINPITYAFV 300 Qy 301 GEKFRNYLLVFFQKTHIAKRFCCKCSIFQQEAPERASSYTRSTGEQESVGL 352

Db 301 GEKFPRNLLVFQKHTAKRPFCKCCSFQQEAPRASSVYTRSTGEQESVGL 352

RESULT 8

US-09-939-226B-5

Sequence 5, Application US/09939226B

Patent No. 600447

GENERAL INFORMATION:

APPLICANT: Euroscreen S.A.

APPLICANT: PARMENTIER, Marc

APPLICANT: VASSART, Gilbert

APPLICANT: LIBERT, Frederick

TITLE OF INVENTION: Methods for Identifying Compounds which Bind the Active CCR5 Chem

FILE REFERENCE: Receptor

FILE REFERENCE: 9409/2023C

CURRENT APPLICATION NUMBER: US/09/939, 226B

CURRENT FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: US 08/833, 752

PRIOR FILING DATE: 1997-04-09

PRIOR APPLICATION NUMBER: US 09/626, 939

PRIOR FILING DATE: 2000-07-07

PRIOR APPLICATION NUMBER: US 08/810, 028

PRIOR FILING DATE: 1997-03-04

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin version 3.1

SEQ ID NO 5

LENGTH: 352

TYPE: PRT

ORGANISM: Homo sapiens

US-09-939-226B-5

Query Match 99.7%; Score 1836; DB 4; Length 352;

Best Local Similarity 99.7%; Pred. No. 1.e-146;

Matches 351; Conservative 0; Mismatches 0; Gaps 0;

Indels 0; Gaps 0;

Qy 1 MDYQVSSPIVDINYTSEPCOKINVQIARLPLLYSLVFIGFVGNNMLVILILINCKR 60

Db 1 MDYQVSSPIVDINYTSEPCOKINVQIARLPLLYSLVFIGFVGNNMLVILILINCKR 60

Qy 61 LKSMTDYLNLALISDLFFLITVTPWAHYLAQNDFGNTMCQLLTGLYFIGFSGIFIFI 120

Db 61 LKSMTDYLNLALISDLFFLITVTPWAHYAAQNDFGNTMCQLLTGLYFIGFSGIFIFI 120

Qy 61 LKSMTDYLNLALISDLFFLITVTPWAHYAAQNDFGNTMCQLLTGLYFIGFSGIFIFI 120

Db 61 LKSMTDYLNLALISDLFFLITVTPWAHYAAQNDFGNTMCQLLTGLYFIGFSGIFIFI 120

Qy 121 LLTIDRYLAVHAYAFLKARTTFCGTTSVITWWAVASLPGLITFSGIFLTKLRLRNEKRRHRAVLIFTI 180

Db 121 LLTIDRYLAVHAYAFLKARTTFCGTTSVITWWAVASLPGLITFSGIFLTKLRLRNEKRRHRAVLIFTI 180

Qy 181 HFPYSQYQFWKNFQTLKIVLGLVPLVMVICSGILKTLRLRNEKRRHRAVLIFTI 240

Db 181 HFPYSQYQFWKNFQTLKIVLGLVPLVMVICSGILKTLRLRNEKRRHRAVLIFTI 240

Qy 181 HFPYSQYQFWKNFQTLKIVLGLVPLVMVICSGILKTLRLRNEKRRHRAVLIFTI 240

Db 181 HFPYSQYQFWKNFQTLKIVLGLVPLVMVICSGILKTLRLRNEKRRHRAVLIFTI 240

Qy 241 MIVYFLWAPYNNVILLNTFOEFFGLNNCSSSNRLDQAMQVTETLGTMTCINPIIYAFV 300

Db 241 MIVYFLWAPYNNVILLNTFOEFFGLNNCSSSNRLDQAMQVTETLGTMTCINPIIYAFV 300

Qy 241 MIVYFLWAPYNNVILLNTFOEFFGLNNCSSSNRLDQAMQVTETLGTMTCINPIIYAFV 300

Db 241 MIVYFLWAPYNNVILLNTFOEFFGLNNCSSSNRLDQAMQVTETLGTMTCINPIIYAFV 300

Qy 301 GEKFPRNLLVFQKHTAKRPFCKCCSFQQEAPRASSVYTRSTGEQESVGL 352

Db 301 GEKFPRNLLVFQKHTAKRPFCKCCSFQQEAPRASSVYTRSTGEQESVGL 352

RESULT 9

US-09-045-583-52

Sequence 52, Application US/09045583

Patent No. 6287805

GENERAL INFORMATION:

APPLICANT: Graham, Gerard J. et al.

TITLE OF INVENTION: No. 6287805e1 Molecules of the G Protein-Coupled

RESONDENCE ADDRESS: NUMBER OF SEQUENCES: 56

ADDRESSEE: LAHIVE & COCKFIELD, LLP

STREET: 28 State Street

CITY: Boston
STATE: Massachusetts
COUNTRY: USA

Z.P.: 0109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/045 583

FILING DATE: 20-MAR-98

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Mantragouras, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: MN1-044

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 742-4114

INFORMATION FOR SEQ ID NO: 52:

SEQUENCE CHARACTERISTICS:

LENGTH: 352 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

US-09-045-583-52

Query Match 99.4%; Score 1830; DB 3; Length 352;

Best Local Similarity 99.1%; Pred. No. 3.6e-146;

Matches 349; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDYQVSSPIVDINYTSEPCOKINVQIARLPLLYSLVFIGFVGNNMLVILILINCKR 60

Db 1 MDYQVSSPIVDINYTSEPCOKINVQIARLPLLYSLVFIGFVGNNMLVILILINCKR 60

Qy 61 LKSMTDYLNLALISDLFFLITVTPWAHYLAQNDFGNTMCQLLTGLYFIGFSGIFIFI 120

Db 61 LKSMTDYLNLALISDLFFLITVTPWAHYAAQNDFGNTMCQLLTGLYFIGFSGIFIFI 120

Qy 61 LKSMTDYLNLALISDLFFLITVTPWAHYAAQNDFGNTMCQLLTGLYFIGFSGIFIFI 120

Db 61 LKSMTDYLNLALISDLFFLITVTPWAHYAAQNDFGNTMCQLLTGLYFIGFSGIFIFI 120

Qy 121 LLTIDRYLAVHAYAFLKARTTFCGTTSVITWWAVASLPGLITFSGIFLTKLRLRNEKRRHRAVLIFTI 180

Db 121 LLTIDRYLAVHAYAFLKARTTFCGTTSVITWWAVASLPGLITFSGIFLTKLRLRNEKRRHRAVLIFTI 180

Qy 181 HFPYSQYQFWKNFQTLKIVLGLVPLVMVICSGILKTLRLRNEKRRHRAVLIFTI 240

Db 181 HFPYSQYQFWKNFQTLKIVLGLVPLVMVICSGILKTLRLRNEKRRHRAVLIFTI 240

Qy 181 HFPYSQYQFWKNFQTLKIVLGLVPLVMVICSGILKTLRLRNEKRRHRAVLIFTI 240

Db 181 HFPYSQYQFWKNFQTLKIVLGLVPLVMVICSGILKTLRLRNEKRRHRAVLIFTI 240

Qy 241 MIVYFLWAPYNNVILLNTFOEFFGLNNCSSSNRLDQAMQVTETLGTMTCINPIIYAFV 300

Db 241 MIVYFLWAPYNNVILLNTFOEFFGLNNCSSSNRLDQAMQVTETLGTMTCINPIIYAFV 300

Qy 301 GEKFPRNLLVFQKHTAKRPFCKCCSFQQEAPRASSVYTRSTGEQESVGL 352

Db 301 GEKFPRNLLVFQKHTAKRPFCKCCSFQQEAPRASSVYTRSTGEQESVGL 352

RESULT 10

US-09-514-185-52

Sequence 52, Application US/09534185

Patent No. 6403167

GENERAL INFORMATION:

APPLICANT: Graham, Gerard J. et al.

TITLE OF INVENTION: No. 6403167e1 Molecules of the G Protein-Coupled

RESONDENCE ADDRESS: Therefor

NUMBER OF SEQUENCES: 56

ADDRESSEE: LAHIVE & COCKFIELD, LLP

STREET: 28 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/534,185
 FILING DATE: 24-Mar-2000
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/045,583
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Mandragoras, Amy E.
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: MNI-044
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 742-4214
 INFORMATION FOR SEQ ID NO: 52:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 352 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FRAGMENT TYPE: internal
 DESCRIPTION: SEQ ID NO: 52:
 US-09-534-185-52

Query Match 99.4%; Score 1830; DB 4; Length 352;
 Best Local Similarity 99.4%; Pred. No. 3_6e-146;
 Matches 350; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYTTSEPCOKINKVQTAARLIPPLPLSILVFIGFVNMLVILLINCKR 60
 Db 1 MDYQVSSPIYDINYTTSEPCOKINKVQTAARLIPPLPLSILVFIGFVNMLVILLINCKR 60

QY 61 LKSMTDIVLNLAISDLFFLILTYPFWAHYLAAQDFGNTMCQLLTGLYFIGFSSGIPRI 120
 Db 61 LKSMTDIVLNLAISDLFFLILTYPFWAHYLAAQDFGNTMCQLLTGLYFIGFSSGIPRI 120

QY 121 LLTIDRYLAVVHAVALKARTTGFVWTSVITWVAVFASLPGIITFRSQKEGHYTCS 180
 Db 121 LLTIDRYLAVVHAVALKARTTGFVWTSVITWVAVFASLPGIITFRSQKEGHYTCS 180

QY 181 HFPSQYQFWKNFQTLKIVLGLVPLVLYMVCYSGIKLTLRCRNEKRAVRIFTI 240
 Db 181 HFPSQYQFWKNFQTLKIVLGLVPLVLYMVCYSGIKLTLRCRNEKRAVRIFTI 240

QY 241 MIVYFLFWAPNVTLLNTFOERFFGLANCCSSSNRLDQAMQVTETLGMTHCCINPITYAFV 300
 Db 241 MIVYFLFWAPNVTLLNTFOERFFGLANCCSSSNRLDQAMQVTETLGMTHCCINPITYAFV 300

QY 301 GEKFRNYLLVFQKHIAKRFCCKCCSFQEAPEASSYTRSTGEQSIVGL 352
 Db 301 GEKFRNYLLVFQKHIAKRFCCKCCSFQEAPEASSYTRSTGEQSIVGL 352

RESULT 12
 US-09-502-783A-2

Sequence 2, Application US/09502783A.
 Patent No. 6511826
 GENERAL INFORMATION:
 APPLICANT: Li, Yi
 APPLICANT: Rubin, Steven M.
 TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCR
 TITLE OF INVENTION: HDGRN10
 FILE REFERENCE: 1488_115.0006
 CURRENT APPLICATION NUMBER: US/09/502,783A
 CURRENT FILING DATE: 2001-08-23
 PRIOR APPLICATION NUMBER: 08/466,343
 PRIOR FILING DATE: 1995-06-06
 NUMBER OF SEQ ID NOS: 9
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 2
 LENGTH: 352
 TYPE: PPT
 ORGANISM: Homo sapiens
 US-09-502-783A-2

Query Match 99.3%; Score 1828; DB 4; Length 352;
 Best Local Similarity 99.4%; Pred. No. 5.3e-145;
 Matches 350; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYTTSEPCOKINKVQTAARLIPPLPLSILVFIGFVNMLVILLINCKR 60
 Db 1 MDYQVSSPIYDINYTTSEPCOKINKVQTAARLIPPLPLSILVFIGFVNMLVILLINCKR 60

RESULT 11
 US-09-826-509-477

Sequence 477, Application US/09826509
 Patent No. 680654
 GENERAL INFORMATION:
 APPLICANT: Liaw, Chen W.
 APPLICANT: Lehmann-Bruinsma, Karin
 APPLICANT: Lin, I-Lin
 TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
 TITLE OF INVENTION: Protein-Coupled Receptors

RESULT 14
 US-09-339-912A-2
 Sequence 2, Application US/09339912A
 ; General Information:
 ; Applicant: Ruben, Steven, M.
 ; Title of Invention: Antibodies to Human G-Protein Chemokine Receptor HDGNR10 (CCR5 Receptor)
 ; File Reference: 1488-1150003
 ; Current Application Number: 1488-1150003
 ; Current Filing Date: 1999-06-25
 ; Prior Application Number: 09/195,662
 ; Prior Filing Date: 1998-11-18
 ; Prior Application Number: 08/466,343
 ; Prior Filing Date: 1995-06-06
 ; Number of SEQ ID NOS: 9
 ; Software: PatentIn version 3.0
 ; SEQ ID NO: 2
 ; LENGTH: 352
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence: Genomic
 ; FEATUE: OTHER INFORMATION: Deduced Amino Acid Sequence
 ; US-09-339-912A-2

Query 61 LKSMTDIYLLNLAISDLFLLTYPFWAHYLAAQDFGNTMCQQLTGlyFGFSGIFFI 120
 Database 61 LKSMTDIYLLNLAISDLFLLTYPFWAHYLAAQDFGNTMCQQLTGlyFGFSGIFFI 120
 Query 121 LTIDRYLAVVHAYFALKARTVTGVTTSVITWWAVFASLPGLIIFTRSKERGHYTCS 180
 Database 121 LTIDRYLAVVHAYFALKARTVTGVTTSVITWWAVFASLPGLIIFTRSKERGHYTCS 180
 Query 181 HFPYSQYQFWKNQFQLKIVLGVLPLVMVICSYGILKTLRRCNEKEGRHRAVLIFTI 240
 Database 181 HFPYSQYQFWKNQFQLKIVLGVLPLVMVICSYGILKTLRRCNEKEGRHRAVLIFTI 240
 Query 241 MITYFLWAPYNVILLNTFQEFGLNCCSSSRQLDQAMQVTELTGMTHCCINPIIYAFV 300
 Database 241 MITYFLWAPYNVILLNTFQEFGLNCCSSSRQLDQAMQVTELTGMTHCCINPIIYAFV 300
 Query 301 GEKFRNYLIVFFQKHLAKRFCKCCSIFQOEAPERSYYTRSTGEQEISVGL 352
 Database 301 GEKFRNYLIVFFQKHLAKRFCKCCSIFQOEAPERSYYTRSTGEQEISVGL 352

RESULT 13
 US-09-502-784A-2
 Sequence 2, Application US/09502784A
 ; General Information:
 ; Applicant: Li, Yi
 ; Title of Invention: Methods of Screening Using Human G-Protein
 ; File Reference: 1488-1150005
 ; Current Filing Date: 2000-02-11
 ; Prior Application Number: 09/195,662
 ; Prior Filing Date: 1998-11-18
 ; Prior Application Number: 08/466,343
 ; Prior Filing Date: 1995-06-06
 ; Number of SEQ ID NOS: 9
 ; Software: PatentIn Version 3.1
 ; SEQ ID NO: 2
 ; LENGTH: 352
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-502-784A-2

Query Match 99.3%; Score 1828; DB 4; Length 352;
 Best Local Similarity 99.4%; Pred. No. 5.3e-146; Indels 0; Gaps 0;
 Matches 350; Conservative 0; Mismatches 2; Delns 0; Gaps 0;

Query 1 MDYQVSSPYIDINYYTSEPCQKINVQKAARLLPPLYSLVFTFGFVNMLVILLINKR 60
 Database 1 MDYQVSSPYIDINYYTSEPCQKINVQKAARLLPPLYSLVFTFGFVNMLVILLINKR 60
 Query 61 LKSMTDIYLLNLAISDLFLLTYPFWAHYLAAQDFGNTMCQQLTGlyFGFSGIFFI 120
 Database 61 LKSMTDIYLLNLAISDLFLLTYPFWAHYLAAQDFGNTMCQQLTGlyFGFSGIFFI 120
 Query 121 LTIDRYLAVVHAYFALKARTVTGVTTSVITWWAVFASLPGLIIFTRSKERGHYTCS 180
 Database 121 LTIDRYLAVVHAYFALKARTVTGVTTSVITWWAVFASLPGLIIFTRSKERGHYTCS 180
 Query 181 HFPYSQYQFWKNQFQLKIVLGVLPLVMVICSYGILKTLRRCNEKEGRHRAVLIFTI 240
 Database 181 HFPYSQYQFWKNQFQLKIVLGVLPLVMVICSYGILKTLRRCNEKEGRHRAVLIFTI 240
 Query 241 MITYFLWAPYNVILLNTFQEFGLNCCSSSRQLDQAMQVTELTGMTHCCINPIIYAFV 300
 Database 241 MITYFLWAPYNVILLNTFQEFGLNCCSSSRQLDQAMQVTELTGMTHCCINPIIYAFV 300
 Query 301 GEKFRNYLIVFFQKHLAKRFCKCCSIFQOEAPERSYYTRSTGEQEISVGL 352
 Database 301 GEKFRNYLIVFFQKHLAKRFCKCCSIFQOEAPERSYYTRSTGEQEISVGL 352

RESULT 15
 US-09-195-662A-2
 Sequence 2, Application US/09195662A
 ; General Information:
 ; Applicant: Ruben, Steven, M.
 ; Title of Invention: Human G-Protein Chemokine Receptor HDGNR10 (CCR5 Receptor)
 ; File Reference: 1488-1150002
 ; Current Application Number: 1488-1150002
 ; Current Filing Date: 1998-11-18
 ; Prior Application Number: 08/466,343
 ; Prior Filing Date: 1995-06-06
 ; Number of SEQ ID NOS: 9
 ; Software: PatentIn version 3.0
 ; SEQ ID NO: 2

i LENGTH: 352
i TYPE: PRT
i ORGANISM: Artificial Sequence: Genomic
i FEATURE:
i OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-195-662A-2

Qy	Query Match	99.3%	Score 1828;	DB 4;	Length 352;
	Best Local Similarity	99.4%	Pred. No. 5.2e-146;		
Db	Matches 350;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	1 MDYQVSSPIYDINYTSSEPCOKINVQAAARLLPPLKLYPLVIFPGFVNMLVILLINCKR	60			
Db	1 MDYQVSSPIYDINYTSSEPCOKINVQAAARLLPPLKLYPLVIFPGFVNMLVILLINCKR	60			
Qy	61 LKSMTDIYLNLNSDLFFLTVTFWAAHAAQNDFGNTMCQQLTGTLGLYFIGFPGSGIPFTI	120			
Db	61 LKSMTDIYLNLNSDLFFLTVTFWAAHAAQNDFGNTMCQQLTGTLGLYFIGFPGSGIPFTI	120			
Qy	121 LLTIDRYLAVVHAVALKARTVTFGVVTSVITAVAPASLPGLIIFTQSKEGLHYTCSS	180			
Db	121 LLTIDRYLAVVHAVALKARTVTFGVVTSVITAVAPASLPGLIIFTQSKEGLHYTCSS	180			
Qy	181 HFPSQYQPMKNFQTLKIVIGLVLPLVMVICYSGLIKTLRCRNEKCRRAVRLIFTI	240			
Db	181 HFPSQYQPMKNFQTLKIVIGLVLPLVMVICYSGLIKTLRCRNEKCRRAVRLIFTI	240			
Qy	241 MIVYFLFWAPYNIVLLNTPQEFPGLNCSSSRLDQAMQVTETLGMPHCNCINPIIVAFV	300			
Db	241 MIVYFLFWAPYNIVLLNTPQEFPGLNCSSSRLDQAMQVTETLGMPHCNCINPIIVAFV	300			
Qy	301 GEKPRNYLIVFFQKHIAKRFCCKCCSIFQOEAPERASSYTRSTGEQISVGGL	352			
Db	301 GEKPRNYLIVFFQKHIAKRFCCKCCSIFQOEAPERASSYTRSTGEQISVGGL	352			

Search completed: October 3, 2005, 07:48:01
 Job time : 30 secs